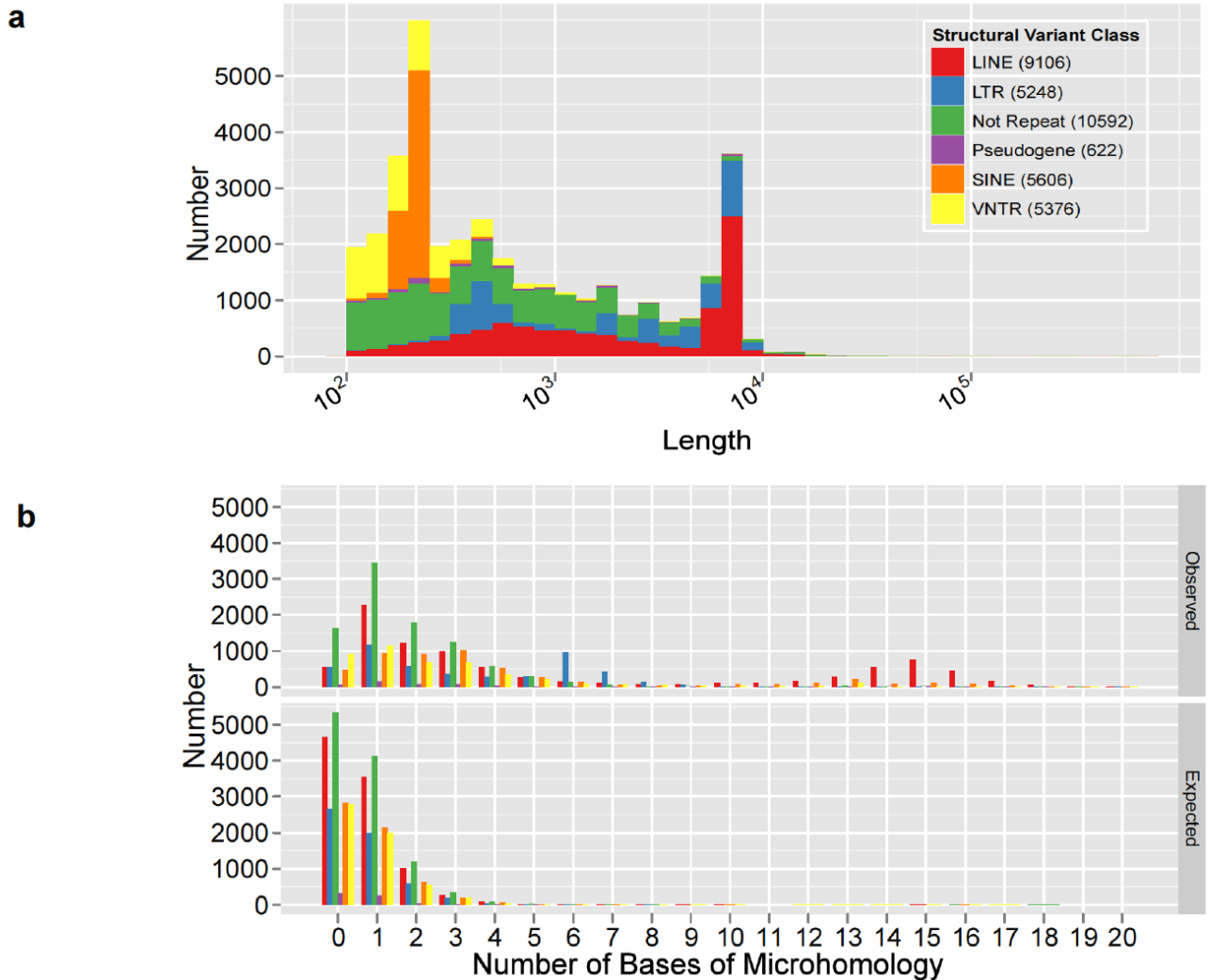# Supplementary Figures

Supplementary Figure 1: Classification of structural variants. **a)** Histogram of lengths for each deletion SV class. **b)** Microhomology surrounding SV breakpoints. SVs were classified as in (a) and the longest length of microhomology between both breakpoints was recorded.

Supplementary Figure 2: Ratio of probe distance in rat to distance in mouse. Histogram of the ratio of the distance between SV probe sequences mapped in the rat genome (Rn4) to the distance between the probes mapped in the mouse genome (mm9). Different SV size classes are indicated by different colors.
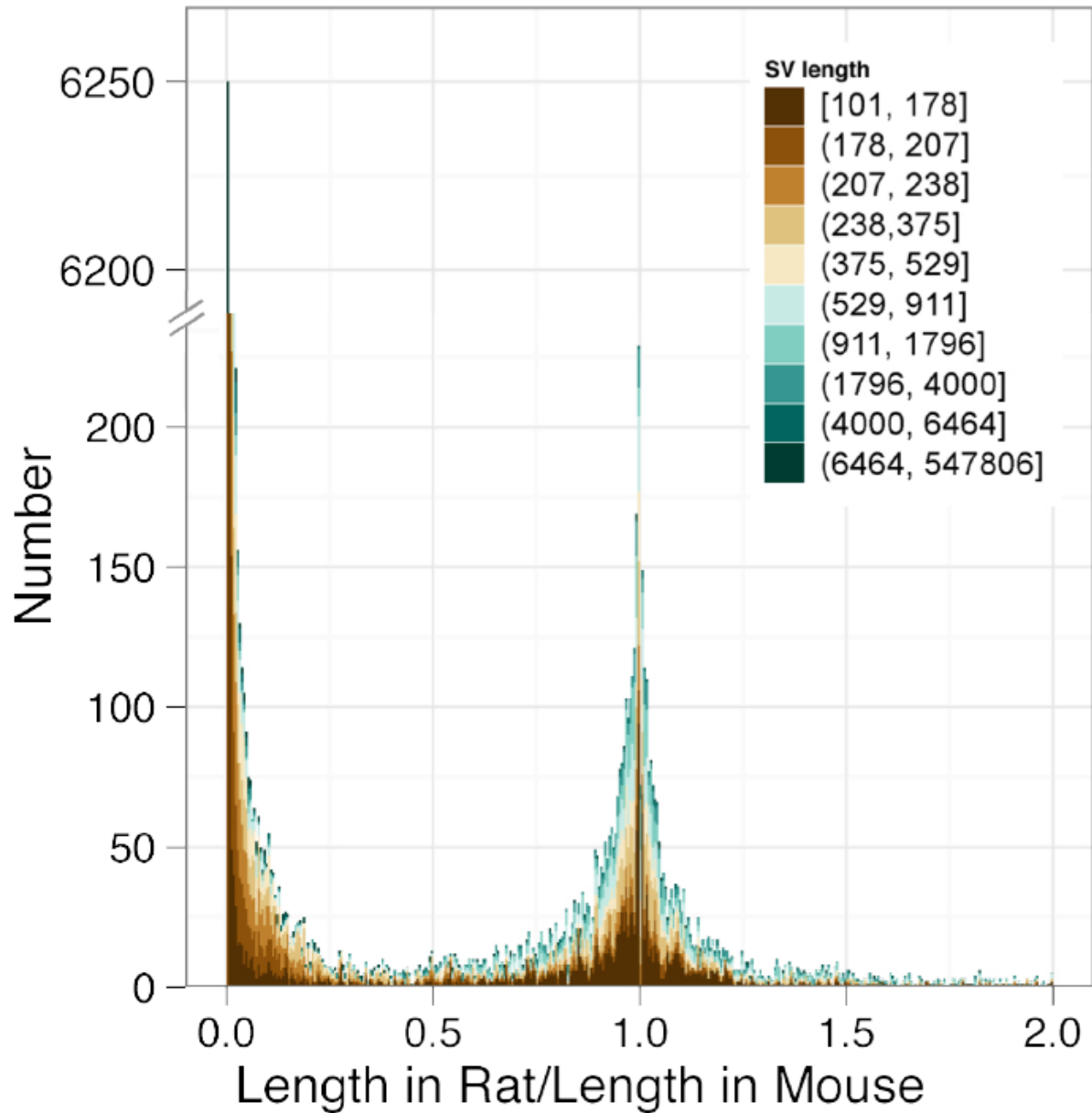
Supplementary Methods

Visual structural variant identification:
We combined visual inspection of short-read sequencing data using LookSeq[31] with molecular validation to improve automated SV detection across the genome. We used two criteria to identify SVs manually: read depth and anomalous paired-end mapping (PEM). We did this using data from the mouse's smallest chromosome (19) in its entirety, and a random set of other chromosomal regions.

Based on read depth and PEM we expected to find eleven patterns that classify SVs. We refer to these as type H ("High-confidence") patterns (H1-H11). In addition, we found ten patterns whose interpretation was ambiguous. We refer to these as type Q ("Questionable") patterns (Q1-Q10).

Investigation of the molecular structure of these PEM patterns is reported in details elsewhere. In brief, **H1_del** is a deletion of a unique sequence; **H2_del** is a deletion of a repeat sequence (*e.g.* LINE, SINE, ERV); **H3_del** is a linked deletion (del-normal-del) where the normal copy is of small size (< 250 bp); **H4_inv** is a simple inversion; **H5_inv** is an inversion with deletion(s); **H6_ins** is an insertion of a unique sequence (*de novo* sequence); **H7_ins** is an insertion of a repeat sequence (*e.g.* LINE, SINE, ERV); **H8_dup** is a tandem duplication; **H9_dup** is an inverted tandem duplication; **H10_dup** is a copy number gain that is neither H8_dup nor H9_dup; **H11_nested** is either a deletion or inversion within a copy number gain; **Q1_del** is a microsatellite size polymorphism; **Q2_del** is a deletion of a unique sequence co-occurring with an insertion; **Q3_del** is a deletion of a repeat sequence co-occurring with an insertion; **Q4_del** is a large deletion; **Q5_del** is a linked insertion; **Q6_del** is a false deletion caused by a retrotransposed pseudogene; **Q7_del** is a VNTR (Variable Number Tandem Repeat); **Q8_inv** is an inversion co-occurring with an insertion; **Q9_inv** is an inverted linked insertion and **Q10_inv** is a false inversion.

Available automated methods to identify SVs are unable to differentiate all these PEM patterns, and may also classify some SVs incorrectly. Therefore we adapted automated methods (see below) to recognize these patterns.

Automatic structural variant detection:
Structural variants (SV) in all inbred strains were detected using four automatic methods: split-read mapping (Pindel)[32], mate-pair analysis (BreakDancer, release-0.0.1r61)[33], single-end cluster analysis (SECluster and RetroSeq, unpublished), and read-depth (CND)[34]. Following merging of these calls into a non-redundant set, computational validation by local assembly and breakpoint refinement was performed for insertions and deletions. Details of the complete pipeline, SVMerge, is described elsewhere[35]. Below is a brief description of the software and the parameters used, any changes to the methods applied specifically for analysis of the 17 mouse strains. Only SVs 100 bp and larger were included in the call sets.

BreakDancerMax, included in the BreakDancer software package, calls SVs by identifying clusters of read pairs with specific alignment signatures. Reads with a mapping quality score of 25 or more were considered, and Fisher's test was used to combine P values from multiple libraries; all other defaults were used. Configuration files for BreakDancerMax were generated from bam2cfg.pl, included in the BreakDancer package. Default values were used, with the exception of the minimal mapping quality, 30. Insertions, deletions and inversions with predicted sizes less than 90 bp and scores less than 25, and with less than 2 supporting read pairs were excluded from further analysis. Any call with 1,000 or more supporting reads was considered an artifact and excluded from further analysis. A small portion of the NOD/SHiLt sequencing was generated from 3 Kb long inserts (resulting in 0.64x coverage), however, these were not used for SV analysis.

Pindel uses a pattern growth method to align reads which span deletion and insertion breakpoints and therefore are unmapped by short read aligners such as MAQ[36] and BWA[37]; the mapped mate is used as an anchor to aid the placement of these reads. The insert size parameter was set to 500 bp. Calls with scores less than or equal to 30 were excluded from further analysis.

SECluster indentifies large *de novo* insertions by searching for adjacent clusters of forward-strand and reverse-strand reads with unmapped mates. A cluster consists of a minimum of 5 overlapping single-end mapped reads, mapped to the same strand, with minimum mapping qualities of 30. Insertion signatures were then identified by comparing the outer coordinates of forward-strand and reverse-strand clusters, allowing up to 100 bp separation, or a 50 bp overlap.

RetroSeq identifies insertions of repeat elements found in Repbase[38]. These insertions are identified from clusters of forward-strand and reverse-strand reads with mates mapped to a Repbase entry, or mapped to a canonical repeat elsewhere in the genome. Alignments of reads to RepBase elements were performed with SSAHA2[39], requiring a minimum hit length of 36 bp and minimum 90% identity.

CND uses a hidden Markov Model and SNP information to analyze changes in read depth to call copy number gain (duplication) or loss. The initial SAMtools[40] pileup step was run with the SNP rate set to 0.001. Prior to calling copy number changes, we applied a GC correction to reads in 1 Kb windows, as described in [41]. CND was run with default values except for the repeat cutoff which was set to 0.35. Posterior probabilities greater than 1×10^{-5} were used to remove unreliable calls. The minimum size considered was 2 Kb for duplications, and 1 Kb for deletions. Heterozygous copy number loss calls were excluded. To identify tandem duplications, we searched all copy number gains for PEM patterns H8_dup and H9_dup. The breakpoints were then modified, using the outer-most coordinates of the read clusters which for the H8_dup and H9_dup PEM patterns.

SV calls made within 650 bp of a reference sequence assembly gap, or overlapping at least 25% of a SV call, were removed to avoid artefacts.

To identify complex PEM patterns, we examined inversion and deletion calls from BreakDancerMax. BreakDancerMax identifies inversions by searching for read pairs mapped to the same strand, separated by a distance greater than the library insert size. However, many of these apparent simple inversions are actually complex SVs, which can be recognized by subtle differences in their PEM patterns. Using in-house Perl scripts to examine BreakDancerMax inversion calls in further detail, we extracted paired end reads from the region of the predicted inversion, and determined the relative positions of forward-strand and reverse-strand clusters (and single-end clusters in Q8_inv). We were able to distinguish between an inversion (H4_inv), inversion plus deletion (H5_inv), inversion plus insertion (Q8_inv), and a linked insertion (Q9_inv). Breakpoints were approximated for inversions, linked insertions and inversion plus insertions by determining the midpoint between forward-strand clusters and reverse-strand clusters. Breakpoints of inversion plus deletion SVs are the outer-most coordinates which are inclusive of the deletion(s). Similarly, re-examination of BreakDancerMax deletion calls allowed us to identify linked deletions (H3_del) and linked insertions (Q5_del). The inner coordinates of the clusters formed by the forward and reverse reads determined the coordinates for each linked deletion.

To generate a non-redundant SV list, non-complex insertions from BreakDancer and Pindel were merged if the predicted insertion coordinates overlapped, and non-complex deletions from BreakDancer, Pindel and CND were merged if the overlap was greater than 75 bp; if the deletion coordinates span 200 bp or more, the coordinates of the intersect of the spans was used to define the SV, otherwise coordinates of the union of the spans were used. All SV types were then combined to generate a list of non-redundant deletions, insertions, inversions, duplications, and complex SVs as listed above. Nested inversions and deletions (H11_nested) were identified by overlapping copy number gains and tandem duplications with simple and complex deletions and inversions. Deletions plus insertions were identified either by merging overlapping deletion and insertion calls (where insertions occur at one of the deletion breakpoints), or by local assembly, described in the next section.

Experimental validation:
Primers were designed using Primer3[42] and purchased from MWG (Germany). Primer design strategy depended on the type and the size of the structural variant. Several independent PCR reactions (at least two) were carried out with Hotstar Taq obtained from Qiagen (Germany). Reactions were performed as previously described[43]. LongRange PCR Kit (Qiagen) was used for genomic region > 2 Kb. PCR gel images were then taken to assess primer design strategy and performance of PCR reaction. Complex and ambigious SV regions were subject to several rounds of primer design and PCR. PCR products were then purified in a 96-well Millipore purification plate resuspended in 30 µl of H_2O and sequenced as previously described[43]. All sequencing reactions were run out on an ABI3700 sequencer and assembled by using PHRED/PHRAP[44].

Assembly of Sanger-based sequencing data:

Consed was used for editing and visualization of the assembly[45]. Strains with the presence and absence of the SV were aligned into one contig. When traces were not available for strains without the SV, we used the reference genome (NCBI m37 mouse assembly) to create a fake trace over the region of interest. Breakpoint analysis of the hand-curated dataset was based on visual inspection of the alignment and BLAT search. The first breakpoint was identified when the strains with and without the SV stopped aligning and the second breakpoint when they started aligning again. Micro-insertion at the breakpoint was defined as any additional sequence present in the strains with the deletion and not in the reference strain. Micro-deletion at the junction was defined as any missing sequence present in the strains with the insertion and not in the reference strain. Breakpoint data are recorded in **Supplementary Table 4**. Most of the time, there were one single pattern of sequence identity (microhomology) at both breakpoints, but when multiple patterns were seen, we recorded the longest possible microhomology. For blunt ended SV, one set of start and end coordinates were recorded, but in case of an SV with microhomology at SV ends, we recorded the SV so that start and end coordinates were the smallest. BLAT was used to obtain exact start and end coordinate of the SV.

Local assemblies and breakpoint refinement:
In an attempt to computationally validate and determine exact breakpoints for deletions, and insertions, *de novo* assembly was performed using Velvet (version 0.7.53)[46] as described in [35]. Assemblies were not performed where the total number of reads exceeded 250,000 in the region of interest, as these are likely to contain unresolvable repetitive regions or artefacts. Contigs resulting from local assembly were aligned to the region of interest in the mouse reference genome using Exonerate[47] and the breakpoints were determined by parsing the alignment output as described in [35]. Where local assembly failed to identify deletion breakpoints, the read depth and repeat content of the predicted deletion was determined, and the deletion call was retained, with the raw deletion breakpoint coordinates, if a decrease in depth was observed.

Strain distribution patterns:
For each SV the strain distribution pattern was determined by first sorting the SVs from all strains by chromosome and start coordinate. Because breakpoint coordinates can differ either due to inaccuracy of breakpoint prediction or due to real differences between strains, we classified SVs from different strains with overlapping coordinates using the following rules: SVs were merged if each had start and stop coordinates spanning 350 bp or more, and a size difference less than 2 times the size of the smaller SV; the outer most coordinates were used to define the SV Otherwise the SVs were considered to be different alleles. SVs less than 350 bp were merged if there was any overlap. Insertions were merged if the breakpoints were within 50 bp.

Sensitivity and specificity analyses:
We established false positive and false negative rates for the automated analysis in three ways.
First, we used our manually identified set of SVs on chromosome 19 where we found 1,017 deletions (756 type H and 261 type Q), 15 inversions (2 type H and 13 type Q)

and three copy number gains (all type H). False negative rates per strain range from 15% to 20% (**Supplementary Table 2a**).

Manual assessment of all H1, H2 and H3 patterns along chromosome 19 in the four wild-derived inbred strains indicates that the false negative rate in these strains is 24% (**Supplementary Table 2b**). This compares to 17% in the laboratory strains. Furthermore the accessible genome for the wild strains is less than for classical strains (23% of Spretus is inaccessible) and this may affect the ratio (if the inaccessible genome has relatively more structural variants than the accessible, which is likely, then we are underestimating the number of SVs in the wild strains). The false positive rates range from 3.7% to 4.8% (**Supplementary Table 2c**).

Second, to ensure that our sensitivity and specificity analyses were not vitiated because we used chromosome 19 as a training set for the automated analysis, we derived a second, smaller, set of manually curated deletions from a randomly chosen 10 Mb region (101 Mb to 111 Mb) from chromosome 3 in strain C3H/HeJ. Automated analysis of this region correctly identified 43/49 (87.7%) and called 2 false positive deletions (4.1%).

Third, we investigated the false negative rate for the automated detection of deletions across the genome using a PCR validation dataset of 370 simple deletions. Consistent with the chromosome 19 and chromosome 3 analyses we found that the false negative rate for deletions was between 6% and 11%, respectively (**Supplementary Table 3a**).

Few non-deletion SVs were manually detected on chromosome 19, so we turned to PCR-based validation of insertions, inversions and tandem duplications (n = 106 to n = 136 SVs per strain). We found that the average false negative rate was higher than for deletions, ranging from 24% to 31% per strain (**Supplementary Table 3b**). Automated analysis was less successful in detecting the more complex rearrangements, with 35% to 54% false negative rates (n = 33 to n = 41 per strain), however, excluding SVs with Q2 and Q3 PEM patterns, the rates range from 5% to 35% (n= 18 to n= 24 SVs per strain).

In determining false negative rates, manually annotated or PCR-confirmed SVs were compared to automated SV calls. SVs without any overlap with an automated SV call were counted as false negatives. Similarly, false positives on chromosome 19 and the 10 Mb region of chromosome 3 were those automated SV calls without any overlap with a manually annotated SV call. The accuracy of the breakpoints was assessed independently. To call a match for insertions, we allowed a window of 50 bp on either side of the insertion breakpoint. Minimum size predictions from automated SV calling were limited to 100 bp; however, to allow for some error in the SV size prediction from manual annotation, manually annotated SVs predicted to be at least 50 bp in size were used in the false positive and false negative calculations. Where the exact breakpoint was determined from PCR and Sanger-based sequencing, only SVs 100 bp or larger were used.

Identification of SVs smaller than 100 bp:

It proved difficult to obtain robust estimates of SVs smaller than 100 bp. We generated SV calls using both Pindel[32] and Dindel[48]. Across the whole genome, we found a total of 151,458 small deletions. We validated this set by visual inspection along the whole of chromosome 19, using a lower bound of 30 bp, because below this size visual inspection becomes difficult. We thus found a false positive rate of about 14%. We then inspected a total of 7.2 Mb of chromosome 19 (3.2-5.6 Mb, 10-12.4 Mb and 58.5-61.2 Mb) and found that a large number of manual calls between 30 and 100 bp were missed by the automated methods (67/75). We confirmed by PCR that the 75 deletions found by manual inspection are in all cases real and smaller than 100 bp. However, the automated methods also identified 42 deletions missed by visual inspection that we confirmed to be real.

Breakpoint accuracy:

Breakpoint accuracy of automated SV calls was determined by comparison to breakpoints of SVs validated by PCR and Sanger sequencing. Comparisons were made with both breakpoints determined by local assembly and refinement (refined deletions and insertions), and breakpoints approximated by PEM analysis only (all SV types). For SV breakpoints determined by local assembly and refinement, micro-homology at the breakpoint affects where the break in the alignment is placed. To account for this, if a refined automated SV call had 5' and 3' breakpoints both upstream or both downstream of the actual coordinates by the same number of bases, then the automated SV call was considered to be an exact match.

Outgroup Analysis:

We made a non-redundant set of SVs by first taking all deletion SVs in the 13 classical strains relative to the reference genome for which we had *de novo* assemblies supporting the breakpoint coordinates. All SVs which did not overlap the coordinates of a SV in another strain were immediately added to the non-redundant set ('private' SV). If an SV overlapped one or more SV in other strains, a strain was picked at random to contribute a representative SV to the non-redundant set. The non-redundant set of relative deletion SVs comprised 36,807 SVs.

We determined the ancestral formation event for each SV by using rat as an outgroup. We took probe sequences of 50 bp in length from 20 bp outside each predicted breakpoint and using the NCBI liftOver tool to find their homologous coordinates in the Rn4 *Rattus Norvegicus* genome[49]. We iteratively tried probes which were located from 20 to 640 bp outside the SV breakpoints, doubling the distance each time. We found 27,833 SVs for which the probe sequences were found on the same chromosome of the Rn4 genome within a threshold distance equal to twice the distance between them in the mm9 genome. When visualized (**Supplementary Fig. 2**) the SVs which did not overlap VNTRs cleanly separated into two groups representing historical deletion events and historical insertions into the reference genome. We found the clustering was not possible from SVs which contained a large proportion of VNTRs and we were not able to determine ancestral event for these SVs (data not shown). We defined each SV

as an ancestral deletions if the distance between the probes in the rat genome was greater than half that in the mouse genome, and as an ancestral insertion otherwise.

We examined 40 of the 8,974 SVs whose probes did not map to the rat sequence and tried to assign ancestral event using Mus spretus sequence reads by manual curation. We found 12 deletions and 24 insertions, which was similar to the genome wide average and suggested there would be no bias if we exclude the indeterminate results in downstream analyses.

Classification of SVs and inferred mechanism:
We first identified SVs likely to have been created via NAHR by recording if the breakpoints of the SV abutted regions of more than 200 bp with 90% or greater sequence identity. We then identified SVs derived from pseudogenes and VNTRs if they were covered by more than 50% of their length by elements annotated as a pseudogene in ensembl 58 or as a VNTR in the SimpleRepeats track of the UCSC genome browser (http://genome.ucsc.edu). We attempted to classify the rest of the SVs into transposon-mediated or non-repeat mediated SVs. Since most of the mouse genome is covered with transposons it was not trivial to identify those SVs which had been caused by the insertion of a transposon. However, since the resolution of the breakpoint coordinates was very high we could make use of the fact that a SV that was genuinely derived from a transposon will generally have breakpoints very close to the endpoints of the annotated transposon.

We used a machine learning procedure to decide whether a SV was caused by the insertion of a transposon. We first defined sequence features based on the known biology of transposon insertion. First we took the transposon class that covered more of the SV than any other and classed it as the 'candidate transposon'. We defined features as a) the proportion of the SV overlapped by the candidate transposon; b) the distance between each breakpoint of the SV and the start and end of the transposon; c) the proportion of the candidate covered by the SV; d) the length of the longest poly-A or poly-T sequence in the region 50 bases around each breakpoint (this was to help detect insertions by the LINE-1 machinery) and finally e) the length of the SV.

To train the classifier, we needed to assign labels giving the 'ground truth' for each SV. We trained a random forest classifier using ancestral insertion or deletion status as labels, treating ancestral event as a 'noisy' label for retrotransposon-mediated SVs[50]. We chose a random forest as a classifier since random forests are able to cope with substantial amounts of noise in the labeling of training data. Furthermore, with only five features and over twenty thousand SVs as training data we were very unlikely to suffer from overfitting the model.

Our trained random forest classifier categorized all SVs with a 6% misclassification rate, measured using Out-of-Bag samples, which is equivalent to using cross-validation using held-out data[51]. If the SV was classified as transposon-mediated we assigned it the class of the candidate transposon. We compared the random forest prediction to 50 SVs that had been hand-curated and in all 50 cases the predictions agreed. We

concluded that the random forest prediction was at least as accurate as a trained human expert in classifying SVs.

Microhomology detection:
We found the longest stretch of sequence that was directly repeated between both breakpoints of each SV. We took 50 bp either side of each breakpoint and determined the length of longest substring common to both breakpoints that started or ended exactly at a breakpoint.

Analyses of the phenotypic effects of SVs:
We used two sources of expression data for our analysis of the effect of SVs on gene expression: transcript abundance measured in hippocampus, liver and lung using an Illumina oligonucleotide array and RNA seq from whole brain. The former is described in [52]. The latter was generated for this study by sequencing RNA extracted from three individuals of 13 strains: A/J, AKR/J, BALB/cJ, CBA/J, C57BL/6J, C3H/HeJ, DBA/2J, LP/J, NZO/HlLtJ NOD/ShiLtJ, PWK/PhJ, WSB/EiJ and SPRET/EiJ. BAM files were converted to FASTQ files and TopHat [53] was deployed to map data from each library to the genome including splice sites annotated in Ensembl and UCSC gene structures, known mRNAs, and expressed sequence tags, and to exhaustively search for novel splice sites. Once splice sites were defined at the library level TopHat was re-run combining all splice sites from all libraries across all of the strains so that reads from all of the libraries had the opportunity to map over the same splice sites. Cufflinks[54] was then used to quantify expression of all Ensembl genes/transcripts across all libraries and gene models were generated for each strain. Cuffcompare was then used to build a set of consensus transcripts, which were used to quantify expression of every RNA-seq-based transcript in each strain. Cuffdiff was then used to identify significant differences in transcript isoform abundance, expression at the gene level, TSS usage, and coding sequence (Ensembl models only).

To assess the effect of SVs on quantitative trait loci (QTLs) we used phenotypes from[55].

Our test of gene function, described in[56], can be briefly summarized as follows: we test whether the strain distribution pattern (SDP) of each variant across the founders of the heterogeneous stock is consistent with the estimated trait values for the founders. To do so, we compare the fit of a QTL linear model in which each founder strain can take a different trait value to one in which those founders that share the same variant allele, are constrained to take the same value. We refer to this as a merge analysis because the alleles that are identical by state are combined, or merged. The statistic is the logP of the ANOVA of the merged model.

Variant imputation was carried out as follows: we apply an HMM-based method[57] to impute genotypes in the set of mice for which they are missing. This procedure results in a posterior probability for each allele at each missing genotype. Leave-one-out analysis showed that when the posterior probability is greater than 98% the accuracy of the imputation method is 99.7%.

Variances of expression data were calculated using ANOVA in the statistical software R using the anova() function on a linear model fitted with the lm() function. We calculated the variance attributable to an SV as described in [28]. For ease of reference the formulae for this method are given below:

B – sum of sum of squares between strains with no SV
W - sum of sum of squares within strains with no SV
b – sum of sum of squares between strains with an SV
w - sum of sum of squares within strains with an SV
P = B/(B+W);
P = b/(b+w);
q = w*P/(1-P);
r = b-q;
Proportion of the variance attributable to an SV = r/(b+w);
We also calculated the variance at each locus by using comparing a model where expression value is explained by the strain to a model in which the expression is explained by strain and whether or not the an animal has the SV. The R code for this is given below:
anova(lm(w$expression.score~1),
lm(w$expression,score~w$sv.strain.status),
lm(w$expression.score~w$strain+w$sv.strain.status))

The mean values across all loci gave a similar result for the contribution of SVs to genetic expression variance to that obtained by partitioning variances as described in [58].

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Supplementary Tables

Supplementary Table 1a

Strain	Total	Simple SVs				Complex SVs		
		del	gain	inv	ins	del+ins	nested	inv+del/ins
129P2/OlaHsd	32227	16292	57	74	15604	105	27	68
129S1/SvImJ	29153	17307	70	88	11516	73	32	67
129S5/SvEvBrd	25340	16089	72	67	8970	43	41	58
A/J	28691	16190	69	92	12184	61	28	67
AKR/J	30742	15806	88	89	14576	88	13	82
BALB/cJ	25702	14859	82	87	10551	48	17	58
C3H/HeJ	28532	16062	94	94	12100	90	16	76
C57BL/6NJ	431	164	44	6	213	0	3	1
CAST/EiJ	86322	50978	361	224	34122	133	239	265
CBA/J	28183	16996	79	83	10867	64	16	78
DBA/2J	28346	17478	67	83	10559	55	29	75
LP/J	30024	16964	64	88	12745	64	30	69
NOD/ShiLtJ	30605	17047	51	115	13244	53	16	79
NZO/HILtJ	25125	15429	62	71	9445	33	23	62
PWK/PhJ	90125	54147	96	272	35098	184	60	268
SPRET/EiJ	157306	91295	112	470	64304	463	110	552
WSB/EiJ	35066	22154	88	97	12521	64	37	105

Structural variants greater than 100 bp in 17 inbred strains

Supplementary Table 1b

Strain	Bases	% of genome
129P2/OlaHsd	36,020,865	1.36
129S1/SvImJ	35,903,624	1.36
129S5/SvEvBrd	33,660,534	1.28
A/J	36,725,371	1.39
AKR/J	33,788,325	1.28
BALB/cJ	34,672,829	1.31
C3H/HeJ	35,104,320	1.33
C57BL/6NJ	2,341,810	0.09
CAST/EiJ	105,596,881	4.00
CBA/J	36,818,508	1.40
DBA/2J	39,111,772	1.48
LP/J	36,099,437	1.37
NOD/ShiLtJ	33,265,218	1.26
NZO/HlLtJ	32,567,448	1.23
PWK/PhJ	96,845,601	3.67
SPRET/EiJ	137,486,655	5.21
WSB/EiJ	51,501,342	1.95

Number of reference bases that lie in structurally variant regions of the genome

Supplementary Table 2a

Strain	Simple deletions (H1,H2,H3,Q1,Q4,Q7)				Excluding Q1 and Q7			
	Found	**Total**	**Overlap**	**FNRate**	**Found**	**Total**	**Overlap**	**FNRate**
A/J	375	504	0.74	0.26	328	404	0.81	0.19
AKR/J	332	479	0.69	0.31	303	370	0.82	0.18
BALB/cJ	379	519	0.73	0.27	344	415	0.83	0.17
C3H/HeJ	359	519	0.69	0.31	325	408	0.80	0.20
C57BL/6N	0	0	N/A	N/A	0	0	N/A	N/A
CBA/J	403	555	0.73	0.27	366	438	0.84	0.16
DBA/2J	434	579	0.75	0.25	384	455	0.84	0.16
LP/J	329	443	0.74	0.26	296	348	0.85	0.15

False negative rates of automated SV calling, based on comparison to chromosome 19 manual annotation of deletions. Shown are the total number of deletions from manual annotation ('Total'), the number of these called by automated SV calling ('Found'), and the resulting overlap and false negative rates ('FNRate'). Overall, the portion of deletions position not identified in any strain by automated SV calling is 15.0% when considering all deletions, and 9.2% when excluding Q1 and Q7 deletions.

Supplementary Table 2b

Strain	Deletions (H1,H2,H3)			
	Found	**Total**	**Overlap**	**FNRate**
Wild-derived				
CAST/EiJ	367	482	0.76	0.24
PWK/PhJ	313	397	0.79	0.21
SPRET/EiJ	325	417	0.78	0.22
WSB/EiJ	253	349	0.72	0.28
HS founders				
A/J	325	400	0.81	0.19
AKR/J	302	369	0.82	0.18
BALB/cJ	341	411	0.83	0.17
C3H/HeJ	323	404	0.80	0.20
CBA/J	365	436	0.84	0.16
DBA/2J	383	453	0.85	0.15
LP/J	295	347	0.85	0.15

False negative rates of automated SV calling for the wild-derived strains and HS founder strains, based on comparison to chromosome 19 manual annotation of deletions (H1,H2,H3). Shown are the total number of deletions from manual annotation ('Total'), the number of these called by automated SV calling ('Found'), and the resulting overlap and false negative rates ('FNRate').

Supplementary Table 2c

Strain	Total Called	Simple deletions (H1,H2,H3,Q1,Q4,Q7)		Excluding Q1 and Q7	
		False	**FPRate**	**False**	**FPRate**
A/J	404	18	0.045	67	0.17
AKR/J	351	14	0.040	44	0.13
BALB/cJ	403	15	0.037	50	0.12
C3H/HeJ	381	16	0.042	50	0.13
C57BL/6N	3	0	0.000	0	0.00
CBA/J	425	19	0.045	57	0.13
DBA/2J	458	22	0.048	73	0.16
LP/J	345	15	0.043	48	0.14

False positive rates of automated SV calling, based on comparison to chromosome 19 manual annotation of deletions (H1,H2,H3,Q1,Q4,Q7). Shown are the total number of automated deletion calls on chromosome 19 ('Total Called') and the number of incorrect deletion calls ('False').

Supplementary Table 3a

Strain	Simple deletions (H1,H2,H3,Q1,Q4,Q7)				Excluding Q1 and Q7			
	Found	**Total**	**Overlap**	**FNRate**	**Found**	**Total**	**Overlap**	**FNRate**
A/J	178	224	0.79	0.21	162	183	0.89	0.11
AKR/J	158	200	0.79	0.21	142	151	0.94	0.06
BALB/cJ	170	209	0.81	0.19	152	168	0.90	0.10
C3H/HeJ	196	249	0.79	0.21	181	203	0.89	0.11
C57BL/6N	0	1	0.00	1.00	0	1	0.00	1.00
CBA/J	184	229	0.80	0.20	166	182	0.91	0.09
DBA/2J	186	230	0.81	0.19	166	185	0.90	0.10
LP/J	154	198	0.78	0.22	141	158	0.89	0.11

False negative rates of automated SV calling, based on comparison to PCR-validated simple deletions from the genome. Comparisons were made to PCR-validated deletions >100 bp only ('Total'). Shown are the number of these deletions identified by automated SV calling ('Found') and the resulting false negative rates ('FNRate') when compared to all simple deletions, and when excluding deletions with Q1 and Q7 PEM pattern.

Supplementary Table 3b

Strain	Simple SVs				Complex SVs					Total Complex SVs found	Total, excluding Q2 and Q3
	CNG	**Inv**	**Ins**	Total Simple SVs found	**Del+Ins**	**Inv+Ins**	**Inv+Del**	**Nested Del**			
	H8,H9,H10	H4	H6,H7,Q5,Q9		Q2,Q3	Q8	H5	H11(Del in CNG)	Del only		
A/J	6/6	8/8	86/117	100/131	3/20	3/5	5/6	5/9	8/9	19/40	16/20
AKR/J	5/7	5/6	66/97	76/110	1/14	5/5	6/6	4/8	7/8	19/33	18/19
BALB/cJ	5/7	6/6	67/101	78/114	2/19	4/7	5/6	4/9	8/9	19/41	17/22
C3H/HeJ	5/7	9/9	83/120	97/136	4/13	7/7	6/8	4/9	7/9	24/37	20/24
C57BL/6N	0/0	0/0	0/1	0/1	0/0	0/0	0/0	1/3	2/3	2/3	2/3
CBA/J	2/4	5/7	82/115	89/126	3/12	7/8	4/6	3/9	7/9	21/35	18/23
DBA/2J	2/4	7/7	84/111	93/122	2/14	5/8	4/5	4/10	6/10	17/37	15/23
LP/J	4/5	4/6	65/95	73/106	1/16	4/5	6/6	2/7	5/7	16/34	15/18
Total SV sites	16	9	177	202	24	10	14	12	12	60	36

Number of PCR-validated SVs found by automated SV calling.

Comparisons were made to PCR-validated SVs >100 bp only. Shown are the SV types (CNG=copy number gain; Inv=inversion; Ins=insertion; Del=deletion) and associated PEM patterns. The insertions that occur with deletions in the Q2 and Q3 patterns are difficult to identify and are either missed completely or called as deletions only. The numbers in the Del+Ins column are the number called as either Del or Del+Ins. Deletions are called independently of CNGs, and nested deletions are found by overlapping Del and CNG calls. Approximately half of the H11 Dels were found, however when considering the deletion only ('Del only' column) this number increases, indicating that the low overlap is due to missed CNG calls.

Supplementary Table 4

CHR	BP_START	BP_END	BP_LENGTH	PEM_PATTERN	A_J	AKR_J	BALB_cJ	C3H_HeJ	C57BL_6N	CBA_J	DBA_2J	LP_J	SEQed	PRIMER_COVERAGE
1	4791671	4791685	250	H7_ins	0	0	0	1	0	1	1	0	0	1
1	5099477	5104721	5245	H3_del	1	1	1	1	0	1	?	1	0	1
1	7904302	7904691	390	H1_del	1	1	1	1	0	1	0	1	1	1
1	7911924	7912249	326	H2_del	1	1	1	1	0	1	0	1	1	1
1	8217107	8218868	1762	H1_del	1	1	1	1	0	1	1	1	1	1
1	8235254	8236173	920	Q2_del	1	1	1	1	0	1	1	1	0	1
1	8239022	8246006	6985	H2_del	1	1	1	1	0	1	1	1	1	1
1	14330384	14332596	2213	H5_inv	1	1	1	1	0	1	1	1	1	2
1	14330384	14332596	2213	H5_inv	1	1	1	1	0	1	1	1	1	2
1	19620056	19620057	622	H6_ins	1	1	1	1	0	1	0	1	1	1
1	33429543	33429646	104	H4_inv	1	0	0	1	0	0	1	0	1	1
1	34715477	34719346	3870	H1_del	1	1	0	1	0	1	1	0	1	1
1	42629669	42629670	>2000	H7_ins	0	1	0	0	0	0	0	0	0	1
1	63440027	63440089	large	H7_ins	1	1	0	1	0	1	1	1	0	1
1	66949028	66949771	744	Q9_inv	0	2	0	0	0	1	1	1	0	1
1	67335622	67335755	134	H4_inv	1	1	0	1	0	1	1	1	1	1
1	90125368	90127221	1854	H11_nested_del	0	0	0	0	0	0	1	0	1	2
1	90125368	90127221	1854	H11_nested_del	0	0	0	0	0	0	1	0	1	2
1	90126886	90127941	1056	H11_nested_inv	1	1	1	1	1	1	1	1	0	2
1	90126886	90127941	1056	H11_nested_inv	1	1	1	1	1	1	1	1	0	2
1	90189197	90190885	1689	H11_nested_del	1	1	1	1	1	1	1	1	1	1
1	100538748	100540638	1891	H2_del	0	na	0	0	0	0	1	1	1	1
1	113931999	113938031	6033	Q2_del	1	0	1	1	0	1	0	1	0	1
1	119672478	119698603	26126	Q4_del	1	0	0	1	0	1	1	0	0	1
1	121756289	121756290	>2000	H7_ins	0	0	1	0	0	0	0	0	0	1
1	127239492	127240521	1030	Q9_inv	1	1	0	1	0	1	1	0	0	2
1	127239492	127240521	1030	Q9_inv	1	1	0	1	0	1	1	0	0	2
1	130430999	130431183	185	Q8_inv	1	1	1	1	0	1	1	1	0	1
1	144252540	144260553	8014	H2_del	1	0	0	1	0	1	0	0	1	1
1	144267285	144272399	5115	H1_del	1	0	0	1	0	1	0	0	1	1
1	152002118	152002119	1000	H7_ins	1	0	0	1	0	1	1	0	0	1
1	158394620	158401436	6817	H1_del	0	1	0	0	0	0	0	0	0	2
1	158394620	158401436	6817	H1_del	0	1	0	0	0	0	0	0	1	2
1	162004359	162065553	61195	H8_dup	0	0	0	1	0	0	0	0	0	1
1	162157648	162157649	197	H7_ins	0	0	1	0	0	0	1	0	1	1
1	170885986	170885992	398	H6_ins	1	1	0	1	0	0	0	1	1	1
1	173411255	173420100	8846	H2_del	1	1	1	1	0	1	1	1	0	1
1	173466830	173467654	825	H11_nested_del	1	1	1	1	0	1	1	1	0	1
1	173500389	173500806	418	H11_nested_del	1	1	1	1	0	1	1	1	0	2
1	173500389	173500806	418	H11_nested_del	1	1	1	1	0	1	1	1	0	2
1	175158884	175158885	large	H7_ins	1	0	0	0	0	0	0	0	0	3
1	175158884	175158885	large	H7_ins	1	0	0	0	0	0	0	0	0	3
1	175158884	175158885	large	H7_ins	1	0	0	0	0	0	0	0	0	3
1	177296844	177296845	203	H6_ins	1	1	1	1	0	1	1	1	1	1
1	178371666	178393696	22031	H8_dup	1	0	0	0	0	0	0	0	1	1
1	184063332	184063729	398	H2_del	1	1	0	0	0	1	1	0	0	1
1	189254262	189255229	968	H1_del	1	1	1	1	0	0	0	0	1	1
1	190747284	190753756	6473	H2_del	1	1	1	1	0	1	1	1	1	1
2	3887052	3891926	4875	H2_del	0	0	0	0	0	0	0	1	1	1
2	18077669	18077735	250	H7_ins	0	1	0	0	0	0	1	0	0	1
2	46183800	46312472	128673	H9_dup	0	1	0	0	0	0	0	0	0	2
2	46183800	46312472	128673	H9_dup	0	1	0	0	0	0	0	0	0	2
2	54314443	54314444	400	H7_ins	1	1	0	1	0	1	1	0	0	1

2	57641836	57641864	>2000	H7_ins	1	1	0	1	0	1	1	0	0	1
2	62479832	62479833	250	H7_ins	0	0	0	0	0	0	1	0	0	1
2	66766229	66766238	217	H7_ins	0	0	0	1	0	1	1	0	1	1
2	69391437	69391441	150	H7_ins	1	1	0	0	0	0	0	0	0	1
2	70985438	70986650	1213	Q5_del	1	1	0	1	0	0	0	0	0	1
2	74930888	74930889	383	H6_ins	0	0	0	1	0	1	1	0	1	1
2	86179898	86186982	7085	H2_del	1	1	1	1	0	1	1	1	1	1
2	100011323	100015761	4439	H2_del	1	1	1	1	0	1	1	1	1	1
2	100445192	100449478	4287	Q7_del	0	1	1	1	0	1	1	1	1	1
2	113228067	113228166	100	H1_del	0	0	0	1	0	0	0	0	1	1
2	113229898	113230949	1052	H1_del	0	0	0	1	0	0	0	0	1	1
2	113358620	113365020	6401	H2_del	1	1	1	1	0	1	1	0	1	1
2	116881603	116888507	6905	H3_del	0	0	0	1	0	1	0	0	1	1
2	121499987	121499988	250	H7_ins	1	1	1	1	0	1	1	1	0	1
2	123185031	123185308	278	H1_del	1	1	1	1	0	1	1	1	1	1
2	123468549	123469197	649	H1_del	1	0	1	0	0	0	1	0	1	1
2	140309421	140346234	36814	H8_dup	1	0	0	0	0	0	0	0	1	1
2	141668240	141703651	35412	H1_del	0	0	0	0	0	0	1	0	1	2
2	141668240	141703651	35412	H1_del	0	0	0	0	0	0	1	0	1	2
2	144402760	144402971	212	H2_del	0	0	0	0	0	0	1	1	1	1
2	146022210	146024157	1948	H1_del	1	0	1	1	0	1	0	0	1	1
2	152910553	152912192	1640	H1_del	1	0	0	0	0	0	0	0	1	1
2	152944961	152945157	197	H1_del	1	0	0	0	0	0	0	0	1	1
2	154428051	154432173	4123	H8_dup	0	0	1	1	0	1	0	0	0	1
2	157526823	157528253	1431	H4_inv	1	1	1	1	0	1	1	1	0	2
2	157526823	157528253	1431	H4_inv	1	1	1	1	0	1	1	1	0	2
2	162296521	162296673	153	H1_del	0	1	0	0	0	0	1	1	1	1
2	162302046	162302116	71	H1_del	0	0	0	0	0	0	1	1	1	1
2	162553910	162555297	1388	H2_del	0	0	0	0	0	0	1	1	1	1
2	162558277	162559605	1329	H1_del	1	0	1	1	0	1	1	1	1	1
2	171873702	171873703	>2000	H7_ins	1	1	0	0	0	0	0	1	0	1
2	172253836	172305516	51681	H10_dup	0	0	1	0	0	0	0	0	0	1
3	9260353	9261290	938	H5_inv	1	1	1	1	0	1	1	0	1	1
3	19250437	19250460	>2000	H7_ins	1	0	0	1	0	1	0	0	0	1
3	21573985	21573997	225	H7_ins	0	1	0	0	0	1	0	0	0	1
3	34179356	34184704	5349	H1_del	1	0	0	1	0	1	0	0	1	1
3	37113544	37116357	2814	H2_del	1	1	0	1	0	1	1	1	1	1
3	37760731	37760750	150	H7_ins	0	0	0	0	0	0	1	1	0	1
3	37832169	37832344	176	H1_del	1	0	0	1	0	1	0	0	1	2
3	37832169	37832344	176	H1_del	1	0	0	1	0	1	0	0	1	2
3	38290496	38290868	373	Q3_del	1	1	0	1	0	1	1	1	1	1
3	60336031	60336032	1000	H6_ins	1	1	1	1	0	1	1	1	0	1
3	69411081	69411126	125	H7_ins	1	1	1	1	0	1	1	1	0	1
3	70474452	70483924	9473	H2_del	1	1	1	1	0	1	1	1	0	1
3	70485722	70485937	216	H1_del	1	1	1	1	0	1	1	1	1	1
3	70491633	70499594	7962	H3_del	1	1	1	1	0	1	1	1	1	1
3	70522566	70529026	6461	H2_del	1	1	1	1	0	1	1	1	0	1
3	70548190	70551321	3132	H2_del	1	1	1	1	0	1	1	1	1	1
3	74604008	74605021	1014	H2_del	0	1	0	0	0	0	1	1	1	1
3	83121654	83121655	>2000	H7_ins	1	0	0	1	0	1	0	1	0	1
3	87245084	87245947	864	H1_del	0	0	0	0	0	0	0	0	1	1
3	87780530	87780662	133	Q7_del	1	1	1	1	0	1	1	0	0	4
3	87780530	87780662	133	Q7_del	1	1	1	1	0	1	1	0	0	4
3	87780530	87780662	133	Q7_del	1	1	1	1	0	1	1	0	0	4
3	87780530	87780662	133	Q7_del	1	1	1	1	0	1	1	0	1	4
3	91831862	91835385	3524	H1_del	0	0	0	0	0	0	0	0	1	1
3	93063716	93064788	1073	Q5_del	1	0	0	1	0	0	0	1	0	1
3	93377864	93377879	200	H7_ins	1	1	0	1	0	1	1	1	0	1
3	105734154	105735483	1330	Q9_inv	1	0	0	1	0	1	0	0	0	1
3	124109159	124110356	1198	Q9_inv	1	0	1	1	0	1	0	0	0	1
3	124827002	124828417	1416	H5_inv	1	0	1	1	0	1	0	0	1	1
3	126808520	126809348	829	H2_del	1	0	1	1	0	1	0	1	0	1
3	126843801	126850137	6337	H2_del	1	0	1	1	0	1	0	1	0	1
3	126922571	126924090	1520	H1_del	1	0	1	1	0	1	0	1	0	1

3	126938128	126938804	677	H2_del	1	0	1	1	0	1	0	1	1	1
3	127297615	127298657	1043	H1_del	1	0	1	1	0	1	0	1	1	2
3	127297615	127298657	1043	H1_del	1	0	1	1	0	1	0	1	1	2
3	127740121	127740698	578	Q9_inv	1	0	1	1	0	1	0	1	1	1
3	130503459	130503828	370	Q1_del	0	1	0	1	0	0	1	1	0	1
3	138642047	138642228	182	Q1_del	1	1	1	1	0	1	0	1	0	1
3	140351783	140354784	3002	H5_inv	1	1	1	1	0	1	1	0	0	1
3	142263731	142288560	24830	H8_dup	1	0	1	1	0	0	0	1	0	1
3	148975154	148975155	100	H6_ins	1	1	1	1	0	1	1	1	0	1
3	154547755	154548003	249	H2_del	1	0	1	1	0	0	1	0	0	1
4	14519304	14520780	1477	H3_del	1	0	0	0	0	0	0	0	0	1
4	21560566	21561053	488	Q9_inv	1	0	1	1	0	1	1	1	0	1
4	32070457	32072128	1672	H3_del	1	1	1	1	0	1	1	1	0	1
4	49690362	49690363	137	H6_ins	0	0	0	0	0	1	1	0	1	1
4	54639543	54646027	6485	H2_del	1	1	1	1	0	1	1	1	1	1
4	54668271	54674939	6669	H2_del	1	1	1	1	0	1	1	1	1	1
4	54683053	54689756	6704	H2_del	1	1	1	1	0	1	1	1	1	1
4	54708586	54714804	6219	H2_del	1	1	1	1	0	1	1	1	1	1
4	55310563	55310859	400/300	H7_ins	1	1	1	1	0	1	1	2	0	1
4	55506836	55508642	1807	Q9_inv	1	1	1	1	0	1	1	1	0	1
4	56976927	56978597	1671	Q9_inv	1	1	1	1	0	1	1	1	0	1
4	89521955	89521976	>2000	H7_ins	0	0	0	0	0	0	0	1	0	1
4	102503092	102503098	>2000	H7_ins	0	1	0	0	0	0	0	0	0	1
4	108266812	108266813	100/200	H6_ins	2	1	1	1	0	1	1	2	0	1
4	108951263	108951264	6400	H7_ins	1	0	0	0	0	0	1	1	0	4
4	108951263	108951264	6400	H7_ins	1	0	0	0	0	0	1	1	0	4
4	108951263	108951264	6400	H7_ins	1	0	0	0	0	0	1	1	1	4
4	108951263	108951264	6400	H7_ins	1	0	0	0	0	0	1	1	1	4
4	111730456	111736678	6223	H2_del	1	1	1	1	0	1	1	1	1	1
4	111731004	112272814	541811	Q4_del	1	1	1	1	0	1	1	1	0	3
4	111731004	112272814	541811	Q4_del	1	1	1	1	0	1	1	1	0	3
4	111731004	112272814	541811	Q4_del	1	1	1	1	0	1	1	1	0	3
4	111737349	111743558	6210	H2_del	1	1	1	1	0	1	1	1	1	1
4	113837502	113839048	1547	H1_del	1	1	1	1	0	1	1	1	1	1
4	114797988	114798000	250	H7_ins	0	0	1	1	0	1	0	0	0	1
4	118228392	118229637	1246	Q7_del	2	0	1	1	0	1	1	1	0	1
4	118256952	118258063	1112	Q5_del	1	0	1	1	0	1	1	1	0	1
4	118269039	118269247	209	H2_del	1	0	1	1	0	1	1	1	1	1
4	118275150	118277695	2546	H1_del	1	0	1	1	0	1	1	0	1	1
4	124393626	124393627	>2000	H7_ins	1	0	0	0	0	0	0	0	0	1
4	126151361	126151553	193	H2_del	0	0	1	1	0	1	1	0	1	1
4	126153386	126154598	1213	H2_del	1	0	1	1	0	1	1	0	0	1
4	129340598	129341862	1265	H4_inv	1	1	1	1	0	1	1	1	0	2
4	129340598	129341862	1265	H4_inv	1	1	1	1	0	1	1	1	0	2
4	130038388	130038389	202	H7_ins	0	0	0	0	0	0	0	1	1	1
4	136568128	136568377	250	H1_del	1	1	1	1	0	1	1	0	1	1
4	136610614	136610855	242	H1_del	1	1	1	1	0	1	1	0	1	1
4	136866308	136867715	1408	Q9_inv	1	1	1	1	0	1	1	0	0	1
4	138257417	138257954	538	H2_del	0	1	1	1	0	1	1	0	1	1
4	142499810	142500621	812	H1_del	0	1	0	1	0	1	0	0	1	1
4	145158618	145163845	5228	H11_nested_del	1	1	1	1	1	1	1	1	1	1
4	146961660	146967957	6298	H11_nested_del	1	1	1	1	1	1	1	1	1	1
4	147244398	147245739	1342	H1_del	0	1	0	1	0	1	1	1	1	3
4	147244398	147245739	1342	H1_del	0	1	0	1	0	1	1	1	0	3
4	147244398	147245739	1342	H1_del	0	1	0	1	0	1	1	1	0	3
4	148025447	148025771	325	Q9_inv	1	1	1	1	0	1	1	1	0	1
4	148074337	148074345	414/600	H6_ins	2	1	2	1	0	1	2	2	1	1
4	148496626	148496829	204	H2_del	1	1	1	1	0	1	1	1	1	1
5	16218462	16218834	373	Q9_inv	0	0	0	0	0	0	1	0	0	1
5	28927814	28937390	9577	H2_del	1	1	1	1	0	1	0	1	1	1
5	35816744	35816834	91	H4_inv	1	1	1	1	0	1	0	0	1	1
5	49210265	49211452	1188	Q2_del	1	1	1	1	0	1	1	0	0	1
5	49217458	49217662	205	H2_del	1	1	1	1	0	1	1	0	1	1
5	49224513	49224660	148	H1_del	1	1	1	1	0	1	1	0	1	1

5	53159500	53159511	220	H7_ins	1	1	1	1	0	1	1	0	0	1
5	63738213	63738612	400	H2_del	0	0	1	0	0	0	0	0	1	1
5	72878688	72878694	>2000	H7_ins	0	0	0	1	0	1	1	0	0	1
5	73292475	73292557	large	H7_ins	0	0	0	1	0	1	1	0	0	1
5	74086526	74088366	1841	H1_del	0	0	0	1	0	1	1	0	1	1
5	74339123	74342120	2998	H3_del	0	0	0	1	0	1	1	0	1	1
5	75140022	75141012	991	H1_del	0	0	1	1	0	1	1	1	1	1
5	75152281	75156021	3741	H1_del	1	0	1	1	0	1	1	0	1	1
5	87850554	87854999	4446	H1_del	0	0	0	0	0	0	0	1	0	2
5	87850554	87854999	4446	H1_del	0	0	0	0	0	0	0	1	1	2
5	100480298	100481104	807	H3_del	1	1	1	1	0	1	1	1	0	1
5	101286287	101286513	227	H2_del	1	1	1	1	0	1	1	1	1	1
5	101294132	101294515	384	H1_del	1	1	1	1	0	1	1	1	1	1
5	101296700	101296994	295	H1_del	1	1	1	1	0	1	1	1	1	1
5	101300414	101300925	512	H1_del	1	1	1	1	0	1	1	1	1	1
5	101301368	101301563	196	H2_del	1	1	1	1	0	1	1	1	1	1
5	101302256	101302347	92	H1_del	1	1	1	1	0	1	1	1	1	1
5	110779322	110779349	200	H7_ins	1	0	1	0	0	0	1	0	0	1
5	121556617	121556618	1450	H6_ins	1	0	1	1	0	1	0	1	0	1
5	137253268	137253269	245	H7_ins	1	1	1	1	0	1	1	1	1	1
5	138918935	138958166	39232	Q4_del	0	0	0	1	0	1	1	0	0	1
5	142838570	142838836	267	Q8_inv	0	0	0	0	0	1	0	0	0	1
5	148925178	148926218	1041	H5_inv	1	1	1	1	0	0	0	0	1	1
5	148936541	148937099	559	H1_del	1	1	1	1	0	0	0	0	1	1
5	151924065	151926487	2423	H8_dup	0	0	0	0	0	0	0	1	0	1
6	8002992	8006085	3094	H2_del	1	1	0	0	0	0	1	1	1	1
6	34708843	34708844	1600	H6_ins	0	0	0	1	0	1	0	1	0	1
6	46708427	46709510	1084	Q9_inv	1	1	1	0	0	0	0	0	0	1
6	47075660	47119456	43797	Q4_del	1	1	1	1	0	1	1	0	0	1
6	48364360	48364383	200	H7_ins	1	1	1	1	0	1	1	0	0	1
6	50307661	50317358	9698	H8_dup	0	0	0	0	0	0	0	1	1	1
6	50720189	50724196	4008	H1_del	0	1	1	0	0	0	0	0	1	2
6	50720189	50724196	4008	H1_del	0	1	1	0	0	0	0	0	1	2
6	71904866	71911266	6401	H2_del	0	1	0	1	0	1	1	0	0	1
6	72268891	72295181	26291	Q6_del	0	1	0	0	0	0	0	0	0	2
6	72268891	72295181	26291	Q6_del	0	1	0	0	0	0	0	0	0	2
6	72554743	72554744	476	H7_ins	0	0	0	1	0	1	1	0	1	1
6	73310705	73311407	703	Q9_inv	0	1	1	1	0	1	1	0	0	1
6	74424049	74433904	9856	H2_del	0	1	1	0	0	0	0	0	1	1
6	89155469	89163089	7621	H8_dup	0	1	1	0	0	0	0	0	0	1
6	94346302	94346542	>2000	H7_ins	0	0	0	1	0	1	0	0	0	1
6	94987185	94987210	250	H7_ins	1	0	1	0	0	0	1	0	0	1
6	101726204	101734221	8018	H8_dup	1	1	1	1	0	0	1	0	1	1
6	105356596	105364136	7541	H2_del	1	1	1	1	0	1	0	0	1	1
6	109401572	109401576	>2000	H7_ins	0	1	0	1	0	1	1	0	0	1
6	109791807	109792892	1086	H1_del	1	0	1	0	0	0	0	1	0	1
6	116635166	116641587	6422	H2_del	0	1	0	1	0	1	1	1	1	1
6	127924658	127924672	300	H7_ins	1	1	1	1	0	1	1	1	0	1
6	128559593	128559740	148	H2_del	0	0	0	0	0	0	0	0	1	1
6	129689526	129691211	1686	H1_del	0	0	0	0	0	0	0	0	1	2
6	129689526	129691211	1686	H1_del	0	0	0	0	0	0	0	0	0	2
6	129905589	129909799	4211	H1_del	1	1	1	1	0	1	1	1	1	1
6	132580541	132613777	33237	Q4_del	1	1	1	1	0	1	1	1	1	3
6	132580541	132613777	33237	Q4_del	1	1	1	1	0	1	1	1	1	3
6	132580541	132613777	33237	Q4_del	1	1	1	1	0	1	1	1	0	3
6	132985563	132986696	1134	H1_del	0	0	0	0	0	0	0	0	0	2
6	132985563	132986696	1134	H1_del	0	0	0	0	0	0	0	0	1	2
6	133488335	133489905	1571	Q9_inv	1	1	1	1	0	1	1	1	0	1
6	135231391	135237865	6475	H2_del	1	1	1	1	0	1	1	1	1	2
6	135231391	135237865	6475	H2_del	1	1	1	1	0	1	1	1	1	2
6	137972602	137980585	7984	H2_del	0	0	0	0	0	0	0	1	0	1
6	145393326	145393327	400/300	H6_ins	1	1	1	1	0	0	2	1	0	1
6	145409072	145410339	1268	H1_del	0	1	0	1	0	0	1	0	0	1
6	145437565	145442373	4809	H2_del	na	1	na	1	0	0	1	na	1	1

6	145456399	145457122	724	H1_del	0	1	0	1	0	0	1	0	0	1
6	145458156	145458387	232	H2_del	0	1	0	1	0	0	1	0	1	1
6	145480570	145480905	336	H2_del	0	1	0	1	0	0	1	1	1	1
6	145489506	145489507	500	H6_ins	0	1	0	1	0	0	1	0	0	1
6	145490047	145490501	455	H2_del	0	1	0	1	0	0	1	0	1	1
6	145541512	145542036	525	H2_del	0	1	0	1	0	0	1	0	1	1
7	5133612	5133663	>2000	H7_ins	1	1	1	0	0	1	1	1	0	1
7	16995335	16995437	125	H7_ins	0	0	0	1	0	1	1	1	0	1
7	17246703	17253185	6483	H2_del	0	0	0	1	0	1	1	1	1	1
7	18385323	18392140	6818	H2_del	0	1	0	1	0	1	1	1	1	1
7	18573450	18573999	550	H2_del	1	1	1	1	0	1	1	1	1	1
7	28646761	28671650	24890	Q4_del	0	0	0	0	0	0	0	0	1	1
7	31059754	31060025	272	Q9_inv	1	1	1	0	0	0	1	1	0	1
7	37357597	37358443	847	H1_del	1	1	1	1	0	1	0	1	0	1
7	47315836	47316290	455	H2_del	1	1	1	1	0	1	0	1	0	1
7	47345019	47345071	53	H2_del	1	1	1	1	0	1	0	1	1	1
7	47364115	47370665	6551	H2_del	1	1	1	1	0	1	0	1	0	1
7	65133342	65136684	3343	H2_del	0	1	0	1	0	1	0	1	0	1
7	68906690	68906691	large	H7_ins	0	0	0	0	0	0	1	0	0	1
7	69157646	69160446	2801	H2_del	0	0	1	0	0	0	2	0	1	1
7	71233525	71234575	1051	H11_nested_del	0	0	0	0	0	0	1	0	0	1
7	81590762	81590763	950	H6_ins	1	1	1	1	0	1	1	1	0	1
7	90731819	90731820	6400	H7_ins	1	1	1	0	0	0	0	0	1	1
7	92953110	92954752	1643	H4_inv	0	0	0	1	0	1	1	1	1	3
7	92953110	92954752	1643	H4_inv	0	0	0	1	0	1	1	1	1	3
7	92953110	92954752	1643	H4_inv	0	0	0	1	0	1	1	1	1	3
7	101244409	101249387	4979	H8_dup	1	1	1	0	0	0	0	0	0	1
7	106145654	106145655	1000/1500	H6_ins	1	1	1	1	0	2	1	1	0	1
7	106217487	106217488	100/400	H6_ins	1	1	1	2	0	2	2	1	0	1
7	106268087	106268088	550	H6_ins	0	0	0	1	0	1	1	0	0	1
7	106445954	106448591	2638	H2_del	0	0	0	1	0	1	1	0	0	2
7	106445954	106448591	2638	H2_del	0	0	0	1	0	1	1	0	0	2
7	106454826	106455107	282	H1_del	0	0	0	1	0	1	1	0	1	1
7	106459299	106459507	209	H2_del	0	0	0	1	0	1	1	1	1	1
7	111397607	111479433	81827	Q4_del	1	1	1	1	0	1	1	1	1	3
7	111397607	111479433	81827	Q4_del	1	1	1	1	0	1	1	1	0	3
7	111397607	111479433	81827	Q4_del	1	1	1	1	0	1	1	1	0	3
7	111398097	111479997	81901	Q4_del	0	0	0	0	1	0	0	0	0	1
7	111504989	111505193	205	H1_del	1	1	1	1	0	1	1	1	1	1
7	118862052	118862074	>2000	H7_ins	1	1	1	1	0	1	1	1	0	1
7	120410462	120414438	3977	H1_del	0	0	0	1	0	1	1	0	1	2
7	120410462	120414438	3977	H1_del	0	0	0	1	0	1	1	0	1	2
7	140063816	140063821	250	H7_ins	0	1	1	1	0	1	1	0	0	1
7	141430270	141443036	12767	H1_del	0	0	0	0	0	0	1	0	0	1
7	146391456	146391457	145	H7_ins	1	1	1	1	0	0	1	1	1	1
7	146392023	146392189	167	H4_inv	1	1	1	1	0	0	1	1	1	1
7	146435587	146435588	25	H6_ins	1	1	1	1	0	1	1	1	0	1
7	149415121	149415210	90	Q7_del	0	0	1	0	0	0	0	0	1	1
8	13917847	13920412	2566	Q7_del	0	0	0	0	0	0	0	1	0	1
8	19116305	19120037	3733	H2_del	1	0	1	1	0	1	1	1	1	1
8	19447465	19450575	3111	H1_del	1	0	1	1	0	1	1	0	1	2
8	19447465	19450575	3111	H1_del	1	0	1	1	0	1	1	0	0	2
8	24639728	24640312	585	H1_del	0	0	0	0	0	0	0	1	1	1
8	27268894	27273129	4236	Q6_del	1	1	1	1	0	1	1	1	0	2
8	27268894	27273129	4236	Q6_del	1	1	1	1	0	1	1	1	0	2
8	30669981	30670519	539	H2_del	1	1	1	1	0	1	1	1	1	1
8	30962028	30962134	>2000	H7_ins	1	1	1	1	0	1	1	1	0	1
8	31509487	31515680	6194	H2_del	1	1	1	1	0	1	1	1	1	1
8	31578907	31578989	83	H1_del	1	1	1	1	0	1	1	1	1	2
8	31578907	31578989	83	H1_del	1	1	1	1	0	1	1	1	1	2
8	31595128	31595783	656	H2_del	1	1	1	1	0	1	1	1	1	1
8	31997613	31999805	2193	H2_del	1	1	1	1	0	1	1	1	0	1
8	32237946	32237948	391	H6_ins	1	1	1	1	0	1	1	1	1	1
8	38128484	38134853	6370	H2_del	1	1	1	1	0	1	1	1	1	1

8	42427730	42427731	large	H7_ins	1	1	1	1	0	1	1	1	0	1
8	59850269	59852000	1732	H1_del	1	0	0	0	0	1	0	0	0	1
8	66849773	66849791	1400	H7_ins	0	1	1	1	0	1	1	1	0	1
8	74977794	74977795	1000	H6_ins	0	1	1	1	0	1	1	1	0	1
8	77137213	77137760	548	Q8_inv	0	0	1	1	0	1	1	0	0	3
8	77137213	77137760	548	Q8_inv	0	0	1	1	0	1	1	0	0	3
8	77137213	77137760	548	Q8_inv	0	0	1	1	0	1	1	0	0	3
8	77137215	77137732	518	Q8_inv	0	0	1	1	0	1	1	0	0	1
8	83669416	83669417	669	H6_ins	1	0	0	1	0	1	1	0	1	1
8	83946486	83946487	450	H7_ins	1	1	1	1	0	1	1	1	0	1
8	87957244	87957245	500	H7_ins	1	0	0	1	0	1	1	0	1	1
8	93102708	93103040	333	Q9_inv	0	1	1	0	0	1	1	1	0	1
8	93565786	93565983	198	H1_del	0	1	1	0	0	1	1	1	1	1
8	111347703	111347704	150	H6_ins	1	1	1	1	0	1	1	1	0	1
8	118630679	118631013	335	H1_del	0	0	0	0	0	1	1	0	1	1
8	124429324	124429325	1100	H7_ins	1	1	1	1	0	0	0	0	0	1
8	127287825	127290268	2444	H1_del	1	0	1	0	0	0	0	1	0	1
8	127369935	127376353	6419	H2_del	1	1	1	1	0	0	0	0	0	1
8	129687910	129697554	9645	H1_del	0	0	0	0	0	1	1	0	1	1
9	9070853	9072226	1374	H5_inv	0	0	0	0	0	0	0	1	0	1
9	22004856	22005023	168	H1_del	0	0	0	0	0	0	0	1	1	1
9	32815884	32817366	1483	H2_del	0	0	0	0	0	0	1	1	1	1
9	34876572	34876573	1200	H7_ins	1	1	1	1	0	1	1	1	0	1
9	38402589	38403498	910	H1_del	1	1	1	1	0	0	1	0	1	1
9	39158033	39159211	1179	H2_del	0	0	0	0	0	1	0	0	1	1
9	41208037	41208038	50	H6_ins	1	1	1	1	0	1	1	1	0	1
9	47966786	47967163	378	H2_del	1	1	1	1	0	1	1	1	1	1
9	47972404	47972633	230	H1_del	0	0	0	0	0	0	0	1	1	1
9	48007440	48008177	738	H2_del	1	1	1	1	0	1	1	1	1	1
9	55825312	55826965	1654	H1_del	1	1	0	1	0	1	1	1	1	1
9	63437850	63437851	400	H6_ins	1	1	0	1	0	0	0	1	0	1
9	65598577	65598578	450	H7_ins	0	0	0	0	0	0	1	1	0	1
9	65829466	65832813	3348	H1_del	1	1	1	1	0	0	0	1	1	1
9	69816998	69817005	650	H6_ins	1	0	1	1	0	1	1	0	0	1
9	70790321	70790323	250	H7_ins	0	0	0	0	0	0	0	1	0	1
9	80166238	80168302	2065	H3_del	1	1	1	1	0	1	1	1	0	1
9	98366615	98366616	551	H7_ins	1	1	1	1	0	1	1	1	1	1
9	105236054	105243059	7006	H2_del	1	1	1	1	0	1	1	1	0	1
9	105547865	105548006	142	H1_del	1	1	1	1	0	1	1	1	1	1
9	105609003	105609365	363	Q1_del	1	1	1	1	0	1	1	1	1	1
9	105672147	105672822	676	H1_del	1	1	1	1	0	1	1	1	1	1
9	110889280	110889465	186	Q7_del	1	1	1	1	0	1	1	1	0	2
9	110889280	110889465	186	Q7_del	1	1	1	1	0	1	1	1	1	2
9	111153190	111153615	426	H1_del	0	0	0	0	0	1	0	1	1	2
9	111153190	111153615	426	H1_del	0	0	0	0	0	1	0	1	1	2
9	112337311	112337312	>2000	H7_ins	0	0	0	0	0	0	0	1	0	1
9	116169541	116174349	4809	H1_del	1	0	1	1	0	0	0	0	0	1
9	118476504	118491182	14679	Q6_del	0	1	0	1	0	0	0	0	0	2
9	118476504	118491182	14679	Q6_del	0	1	0	1	0	0	0	0	0	2
9	121129353	121148662	19310	H3_del	1	1	1	1	0	1	1	0	0	1
10	3825656	3826051	396	Q9_inv	1	1	1	0	0	0	0	1	0	1
10	7229585	7237495	7911	Q7_del	1	1	1	1	0	1	1	1	0	1
10	8801729	8801730	50	H6_ins	1	1	1	1	0	1	1	0	0	1
10	9908911	9911671	2761	H1_del	1	1	1	1	0	1	0	1	1	1
10	10741720	10741722	233	H6_ins	1	1	1	1	0	1	0	1	1	1
10	12717222	12723714	6493	H2_del	0	0	0	0	0	0	1	0	0	1
10	18087739	18092433	4695	H1_del	1	0	1	1	0	1	1	1	1	1
10	20467348	20467894	547	H1_del	0	1	0	0	0	0	0	0	1	1
10	20473027	20473679	653	H1_del	0	1	0	0	0	0	0	0	1	1
10	21758421	21760395	1975	Q7_del	1	0	1	0	0	0	0	1	0	1
10	23570601	23570602	300	H7_ins	1	1	1	1	0	0	0	0	0	1
10	46614286	46614287	large	H7_ins	0	0	1	1	0	1	1	0	0	1
10	48045544	48046781	1238	H2_del	0	0	1	0	0	0	0	0	0	1
10	62821558	62821559	200	H7_ins	0	0	0	0	0	0	0	1	0	1

10	62971529	62974071	2543	H2_del	0	0	0	0	0	0	0	1	0	1
10	62975365	62981885	6521	H2_del	0	0	0	0	0	0	0	1	0	1
10	63081901	63082728	828	H5_inv	0	0	0	0	0	0	0	1	0	1
10	63125942	63132474	6533	H2_del	0	0	0	0	0	0	0	1	0	1
10	63174518	63175029	512	H5_inv	0	0	0	0	0	0	0	1	1	1
10	63204383	63210721	6339	H2_del	0	0	0	0	0	0	0	1	1	1
10	63250538	63252488	1951	H3_del	0	0	0	0	0	0	0	1	1	1
10	63437444	63438653	1210	Q7_del	0	0	0	0	0	0	0	1	1	1
10	63528576	63530867	2292	H1_del	0	0	0	0	0	0	0	1	1	1
10	63664018	63670857	6840	H2_del	0	0	0	0	0	0	0	1	1	1
10	63856607	63859006	2400	H2_del	0	0	0	0	0	0	0	1	1	1
10	63865597	63865921	325	Q9_inv	0	0	0	0	0	0	0	1	0	1
10	64002264	64004151	1888	H2_del	0	0	0	0	0	0	0	1	1	1
10	81893427	81893451	large	H7_ins	1	1	1	1	0	1	1	1	0	1
10	82048118	82050293	2176	H1_del	1	1	1	1	0	1	1	1	1	1
10	86938749	86939441	693	Q5_del	1	1	1	1	0	1	1	0	0	1
10	88426617	88431075	4459	H2_del	1	1	1	1	0	1	1	1	1	1
10	89517732	89522992	5261	H2_del	0	0	0	0	0	0	1	0	1	1
10	97080464	97085533	5070	H1_del	0	1	0	0	0	0	0	0	1	1
10	99067034	99068050	1017	H1_del	0	1	0	1	0	1	0	0	1	1
10	103498009	103499237	1229	H1_del	1	0	1	0	0	0	1	0	1	1
10	103691728	103696468	4741	H1_del	0	1	0	1	0	1	0	1	1	1
10	104432371	104438855	6485	H2_del	0	1	0	1	0	1	0	1	1	1
10	104483774	104486910	3137	H1_del	1	0	1	0	0	0	1	0	1	2
10	104483774	104486910	3137	H1_del	1	0	1	0	0	0	1	0	1	2
10	106418387	106418496	110	H1_del	1	0	1	1	0	1	1	0	0	1
10	106439396	106439915	520	H3_del	1	0	1	1	0	1	1	0	0	2
10	106439396	106439915	520	H3_del	1	0	1	1	0	1	1	0	0	2
10	107267300	107267520	221	H1_del	1	0	1	1	0	1	1	1	0	1
10	116344222	116360893	16672	Q6_del	0	0	0	0	0	0	0	1	0	2
10	116344222	116360893	16672	Q6_del	0	0	0	0	0	0	0	1	0	2
10	119832611	119832614	250	H7_ins	1	0	1	0	0	0	1	0	0	1
10	123635783	123635784	252	H6_ins	1	1	1	1	0	1	1	0	1	1
11	25027761	25028703	943	Q5_del	1	0	0	1	0	0	1	0	0	1
11	27196067	27199796	3730	H3_del	1	0	0	1	0	0	1	0	1	1
11	27207587	27210070	2484	H2_del	1	0	0	1	0	0	1	0	1	1
11	27277671	27278146	476	H1_del	1	0	0	1	0	0	1	0	1	1
11	28855950	28856765	816	H1_del	1	0	0	1	0	0	1	0	0	1
11	28869029	28875370	6342	H2_del	1	0	0	1	0	0	1	0	1	1
11	28925091	28930829	5739	H2_del	1	1	1	1	0	0	1	1	1	1
11	30276537	30276636	>2000	H7_ins	1	1	1	0	0	1	1	1	0	1
11	30536311	30542763	6453	H1_del	1	0	0	0	0	0	1	0	0	1
11	32479174	32480290	1117	Q7_del	3	4	3	1	0	1	3	3	0	1
11	37565951	37573023	7073	H2_del	0	0	0	0	0	0	1	0	0	1
11	38295032	38300827	5796	H2_del	1	0	1	1	0	1	1	1	1	1
11	46646071	46646072	1102	H6_ins	1	1	1	1	0	1	0	1	1	1
11	54533925	54570045	36121	Q6_del	1	1	1	1	0	1	0	0	0	2
11	54533925	54570045	36121	Q6_del	1	1	1	1	0	1	0	0	0	2
11	60901848	60901853	250	H7_ins	1	0	0	1	0	1	0	0	0	1
11	69096981	69097663	683	Q7_del	0	1	0	0	0	0	0	0	0	1
11	71046193	71101410	55218	Q4_del	0	1	1	1	0	1	1	1	0	6
11	71046193	71101410	55218	Q4_del	0	1	1	1	0	1	1	1	0	6
11	71046193	71101410	55218	Q4_del	0	1	1	1	0	1	1	1	0	6
11	71046193	71101410	55218	Q4_del	0	1	1	1	0	1	1	1	0	6
11	71046193	71101410	55218	Q4_del	0	1	1	1	0	1	1	1	0	6
11	71046193	71101410	55218	Q4_del	0	1	1	1	0	1	1	1	0	6
11	74179316	74203182	23867	H8_dup	0	1	1	1	0	1	1	1	1	1
11	84836199	84836910	712	Q7_del	0	1	0	0	0	0	1	0	0	1
11	87816905	87817370	466	Q9_inv	1	1	1	1	0	1	1	1	0	1
11	88273034	88273064	200	H7_ins	1	1	0	1	0	1	1	1	0	1
11	92743211	92743312	102	Q8_inv	0	0	0	0	0	0	0	1	0	1
11	103370240	103390698	20459	H1_del	0	0	1	0	0	0	0	0	1	1
11	111683248	111683249	50	H6_ins	1	0	1	0	0	1	0	0	0	1
11	112412802	112413602	801	Q9_inv	1	0	0	1	0	1	0	0	0	1

11	115106127	115106250	124	H1_del	0	0	1	0	0	0	0	0	1	1
12	26998661	26998721	61	H1_del	1	1	1	1	0	1	1	1	0	1
12	27029258	27029374	117	H2_del	1	1	1	1	0	1	1	1	0	1
12	27032128	27032356	229	H1_del	1	1	1	1	0	1	1	1	1	1
12	27040459	27040522	64	H1_del	1	1	1	1	0	1	1	1	1	1
12	27046544	27047255	712	H1_del	0	1	0	0	0	0	1	0	1	1
12	27203911	27208747	4837	H1_del	1	1	1	1	0	1	1	1	1	1
12	27233106	27233454	349	H1_del	1	1	1	1	0	1	1	1	1	1
12	27443614	27446916	3303	H1_del	0	1	0	0	0	0	1	0	1	1
12	28724825	28725292	468	H2_del	1	1	1	1	0	1	1	1	1	1
12	28750412	28750710	299	H1_del	1	1	1	1	0	1	1	1	1	1
12	29197920	29197922	353	H6_ins	1	0	1	1	0	1	1	1	1	1
12	29798808	29802312	3505	H1_del	1	1	1	1	0	1	1	0	0	1
12	31759321	31759461	141	Q7_del	1	1	1	1	0	1	0	0	1	1
12	36163830	36166128	2299	H5_inv	0	1	0	0	0	0	1	1	0	1
12	37536566	37537078	513	Q2_del	1	0	1	1	0	1	1	0	0	1
12	37874378	37878614	4237	H2_del	1	0	1	1	0	1	1	0	0	1
12	37881345	37888152	6808	H2_del	1	0	1	1	0	1	1	0	1	1
12	37906873	37907376	504	H2_del	0	0	0	0	0	0	1	0	1	1
12	37917257	37924452	7196	H2_del	0	0	0	0	0	0	1	0	1	1
12	37930820	37937052	6233	H2_del	0	0	0	0	0	0	1	0	1	1
12	49220733	49220748	>2000	H7_ins	1	1	1	1	1	1	0	0	0	1
12	65275455	65280967	5513	H1_del	1	0	1	1	0	1	1	1	1	1
12	67803554	67803575	>2000	H7_ins	1	0	1	1	0	1	0	0	0	1
12	80488619	80488639	200	H7_ins	0	1	0	0	0	0	0	1	0	1
12	93862656	93864069	1414	H5_inv	1	0	0	1	0	0	1	0	1	1
12	94061490	94061511	587	H6_ins	1	0	0	1	0	0	1	0	1	1
12	102832585	102832826	242	H2_del	0	1	1	0	0	1	1	1	0	1
12	107290852	107290855	200	H7_ins	0	0	1	0	0	0	0	0	0	1
12	108556111	108560848	4738	H5_inv	0	0	1	0	0	0	0	0	0	1
12	108582126	108582554	429	H1_del	1	1	1	1	0	1	0	0	1	1
12	111198494	111198495	50	H6_ins	1	0	0	1	0	1	1	0	0	1
12	113554014	113555091	1078	Q5_del	1	1	0	1	0	1	1	0	0	1
12	118453618	118455374	1757	H3_del	1	0	1	1	0	1	0	0	0	1
13	12084528	12085904	1377	H5_inv	0	1	0	0	0	0	0	1	0	1
13	23782488	23782526	200	H7_ins	0	0	0	0	0	0	0	1	0	1
13	35181005	35181380	376	Q8_inv	1	1	1	1	0	1	1	1	0	1
13	47211585	47211586	298	H6_ins	1	0	1	1	0	1	1	1	1	1
13	78259503	78259504	266	H7_ins	0	1	0	1	0	1	1	0	1	1
13	84974150	84980781	6632	H2_del	1	1	1	1	0	1	1	1	1	1
13	96583639	96584969	1331	H1_del	0	1	1	1	0	1	1	0	1	1
13	96778608	96779025	418	H1_del	1	0	0	0	0	0	0	0	1	1
13	100993915	100997513	3599	Q6_del	1	1	1	1	1	1	1	1	0	1
13	101150011	101156395	6385	H11_nested_del	2	1	2	2	0	2	2	0	0	1
13	103980175	103980535	361	H1_del	0	1	1	1	0	1	0	1	0	1
13	109336088	109336089	25	H6_ins	1	0	1	1	0	1	1	1	0	1
13	110907753	110910176	2424	Q9_inv	0	1	0	1	0	1	1	0	0	1
13	113783196	113783359	164	H1_del	1	0	0	0	0	0	0	0	1	1
13	115609852	115610030	179	H1_del	1	1	0	0	0	0	0	0	1	1
13	115707831	115707862	150	H7_ins	1	0	0	0	0	0	0	0	0	1
13	115835117	115835358	242	H2_del	1	0	0	0	0	0	0	0	1	1
13	115836701	115836904	204	H2_del	1	0	0	0	0	0	0	0	1	1
13	116943933	116944422	490	H1_del	1	0	0	1	0	0	1	1	0	1
13	116943950	116944402	453	H1_del	1	0	0	1	0	0	1	1	0	1
13	117221529	117222520	992	H1_del	0	1	1	1	0	1	1	1	0	1
13	117255600	117259080	3481	H2_del	1	1	1	1	0	1	1	1	0	1
13	117291084	117292349	1266	H2_del	1	1	1	1	0	1	1	1	0	1
13	117367749	117373757	6009	H2_del	1	1	1	1	0	1	1	1	0	1
13	117556714	117562765	6052	H1_del	0	na	na	1	0	na	1	1	0	1
13	117626016	117632272	6257	H2_del	1	1	1	0	0	1	0	0	0	1
13	117778706	117778929	224	H2_del	1	0	0	0	0	0	0	0	1	1
13	119049089	119051561	2473	H2_del	1	1	1	0	0	0	0	0	1	1
13	119057811	119058288	478	H2_del	1	1	1	0	0	0	0	0	1	1
13	119062186	119063760	1575	H1_del	1	1	1	0	0	0	0	0	1	1

13	119081799	119082924	1126	H1_del	1	1	1	0	0	0	0	0	1	1
13	119087544	119087994	451	H2_del	1	1	1	0	0	0	0	0	1	1
13	119134049	119135126	1078	H2_del	1	1	1	0	0	0	0	0	1	1
13	120269994	120270679	686	Q9_inv	0	0	0	1	0	1	1	1	0	1
14	47396242	47407971	11730	Q6_del	1	0	1	1	0	1	1	1	0	2
14	47396242	47407971	11730	Q6_del	1	0	1	1	0	1	1	1	0	2
14	48087917	48088295	379	H3_del	1	1	1	0	0	1	1	0	0	1
14	51424736	51424933	198	Q8_inv	1	1	1	1	0	1	1	1	0	1
14	54909261	54909262	large	H7_ins	1	1	1	1	0	1	1	1	0	1
14	61578912	61580777	1866	H11_nested_del	2	1	2	2	0	2	2	2	0	1
14	71238275	71238776	502	H2_del	1	0	1	0	0	0	0	1	1	1
14	71240744	71240859	116	H2_del	1	0	1	0	0	0	0	1	1	1
14	77431662	77431955	294	Q9_inv	1	0	1	0	0	0	0	1	0	1
14	86683899	86684487	589	Q8_inv	1	1	1	1	0	1	1	0	0	1
14	87783636	87783640	>2000	H7_ins	0	1	0	0	0	0	1	0	0	1
14	92627450	92633711	6262	H2_del	1	1	1	1	0	1	0	0	1	1
14	97508958	97512902	3945	H1_del	1	1	1	1	0	1	1	0	1	1
14	101075452	101085425	9974	H2_del	1	1	1	1	0	1	1	2	1	1
14	101077642	101082752	5111	H2_del	2	2	2	2	0	2	2	1	1	1
14	119825968	119826170	203	H2_del	0	0	0	1	0	1	1	1	0	1
15	20187841	20187842	150	H6_ins	1	0	1	0	0	0	1	1	0	1
15	25972850	25972851	>2000	H7_ins	1	0	0	0	0	1	1	1	0	1
15	28411389	28414321	2933	H1_del	0	0	0	1	0	1	1	0	0	1
15	31156193	31156194	large	H7_ins	1	0	0	0	0	0	0	0	0	1
15	46771509	46771510	>2000	H7_ins	1	0	1	0	0	0	0	1	0	1
15	61190214	61190298	800	H7_ins	0	0	1	1	0	1	0	1	0	1
15	64888626	64888628	>2000	H7_ins	0	0	1	1	0	1	0	0	0	1
15	67959554	67959582	1150	H6_ins	0	1	1	1	0	1	1	1	0	1
15	70681438	70687861	6424	H2_del	0	0	0	0	0	0	1	1	1	1
15	70693858	70694038	181	H2_del	0	0	0	0	0	0	1	1	1	1
15	70716744	70717560	817	H2_del	0	0	0	0	0	0	1	1	1	1
15	70725434	70731693	6260	H3_del	0	0	0	0	0	0	1	1	1	1
15	71648584	71648729	146	H11_nested_del	1	0	2	2	0	2	0	0	0	1
15	85811873	85812620	748	Q9_inv	1	1	1	1	0	1	1	1	0	1
15	90958675	90966706	8032	H1_del	1	0	0	1	0	1	1	1	0	2
15	90958675	90966706	8032	H1_del	1	0	0	1	0	1	1	1	0	2
15	90971314	90974384	3071	H3_del	1	0	0	1	0	1	1	1	1	3
15	90971314	90974384	3071	H3_del	1	0	0	1	0	1	1	1	0	3
15	90971314	90974384	3071	H3_del	1	0	0	1	0	1	1	1	0	3
15	91319016	91319999	984	H1_del	0	0	0	0	0	0	0	1	0	1
15	93495180	93495181	447	H7_ins	1	0	0	1	0	1	1	0	1	1
15	98328544	98328861	318	H3_del	1	0	0	1	0	0	0	0	0	2
15	98328544	98328861	318	H3_del	1	0	0	1	0	0	0	0	1	2
15	101786622	101787483	862	Q7_del	1	0	0	1	0	1	0	0	0	1
16	14522606	14522623	>2000	H7_ins	0	0	1	1	0	1	1	0	0	1
16	31737358	31740763	3406	H1_del	0	1	0	1	0	1	1	1	1	1
16	36242912	36243320	409	H2_del	1	0	1	0	0	0	0	1	1	1
16	36244199	36320642	76444	Q4_del	1	0	1	0	0	0	0	1	1	1
16	38869782	38871537	1756	H2_del	1	1	1	1	0	1	1	1	1	1
16	44581956	44581957	large	H7_ins	1	1	1	1	0	1	1	1	0	1
16	45988504	45990548	2045	H1_del	0	0	0	1	0	1	0	0	1	1
16	46016153	46018286	2134	H2_del	0	0	0	1	0	1	0	0	1	1
16	46040340	46040809	470	H2_del	0	0	0	1	0	1	0	0	1	1
16	46077336	46083470	6135	H2_del	0	0	0	1	0	1	0	0	1	1
16	46103583	46106010	2428	H1_del	0	0	0	1	0	1	0	0	1	1
16	47747657	47754129	6473	H2_del	0	0	0	1	0	1	0	0	1	1
16	48298184	48299406	1223	H5_inv	0	0	0	1	0	1	0	0	0	1
16	49332309	49332310	250	H7_ins	0	0	0	1	0	1	0	0	0	1
16	50085097	50089492	4396	H2_del	0	0	0	1	0	1	0	1	1	1
16	66881038	66881353	316	H4_inv	1	0	1	1	0	1	1	0	0	2
16	66881038	66881353	316	H4_inv	1	0	1	1	0	1	1	0	0	2
16	88874294	88874392	99	Q7_del	0	1	0	0	0	1	1	2	1	1
16	93649496	93650617	1122	H2_del	1	1	1	1	0	1	1	1	1	1
17	16694092	16706712	12621	H5_inv	0	0	0	1	0	1	0	0	0	1

17	24104562	24104563	256	H6_ins	1	1	1	1	0	1	1	1	1	1
17	24547569	24550841	3273	Q6_del	0	0	0	0	0	0	1	0	0	2
17	24547569	24550841	3273	Q6_del	0	0	0	0	0	0	1	0	0	2
17	30584323	31061159	476837	H8_dup	1	1	0	1	0	1	1	1	1	2
17	30584323	31061159	476837	H8_dup	1	1	0	1	0	1	1	1	1	2
17	30781375	30781886	512	Q7_del	1	1	1	1	0	1	0	1	0	1
17	30781648	30781883	236	Q1_del	1	1	1	1	0	1	1	1	1	2
17	30781648	30781883	236	Q1_del	1	1	1	1	0	1	1	1	1	2
17	30781660	30781896	237	H11_nested_del	1	1	2	1	0	1	1	1	0	1
17	34483681	34483682	629	H6_ins	1	1	1	1	0	1	1	0	1	1
17	42601227	42601247	>2000	H7_ins	1	1	1	1	0	1	1	1	0	1
17	45309376	45309377	large	H7_ins	1	0	0	0	0	0	0	0	0	1
17	78433695	78434550	856	H2_del	0	0	0	1	0	1	1	0	1	1
17	78459847	78461621	1775	H3_del	0	0	0	1	0	1	1	0	1	1
17	78468447	78475150	6704	H2_del	0	0	0	1	0	1	1	0	1	1
17	78487948	78488586	639	H2_del	0	0	0	1	0	1	1	0	1	1
17	87982636	87982871	236	H1_del	1	0	1	1	0	1	0	0	0	1
17	89956708	89956733	>2000	H7_ins	1	1	1	1	0	1	1	1	0	1
17	91923991	91930215	6225	H2_del	0	1	0	1	0	0	1	1	1	1
18	14490477	14490567	91	H4_inv	1	1	1	1	0	1	0	1	1	1
18	15093458	15093459	200	H7_ins	0	0	1	1	0	1	0	0	0	1
18	17794170	17794304	135	Q8_inv	0	0	0	0	0	0	1	1	0	1
18	35732191	35750122	17932	Q6_del	1	1	1	1	1	1	1	0	0	2
18	35732191	35750122	17932	Q6_del	1	1	1	1	1	1	1	0	0	2
18	35896598	35896906	309	Q9_inv	0	0	0	1	0	0	0	0	0	1
18	39481367	39488964	7598	Q10_inv	1	1	1	1	0	1	1	1	0	3
18	39481367	39488964	7598	Q10_inv	1	1	1	1	0	1	1	1	0	3
18	39481367	39488964	7598	Q10_inv	1	1	1	1	0	1	1	1	0	3
18	51876808	51876809	large	H7_ins	1	0	1	1	0	1	1	0	0	1
18	57817850	57901152	83303	H8_dup	0	1	0	0	0	0	0	0	1	1
18	64607747	64609669	1923	H2_del	0	1	0	0	0	0	0	1	1	1
18	66466493	66466494	>2000	H7_ins	0	1	0	0	0	0	0	0	0	1
18	72226898	72230061	3164	H1_del	1	1	1	1	0	1	1	1	1	1
18	89054604	89054632	>2000	H7_ins	0	0	0	0	0	0	0	1	0	1
19	4310167	4310380	214	H2_del	1	1	1	1	0	1	1	0	0	1
19	4939318	4939715	398	Q7_del	2	2	2	2	0	1	1	0	0	2
19	4939318	4939715	398	Q7_del	2	2	2	2	0	1	1	0	0	2
19	5435940	5436826	887	H2_del	1	1	1	1	0	0	0	0	0	1
19	10141421	10141451	31	H6_ins	1	0	1	1	0	0	0	0	0	1
19	10148784	10148882	99	H1_del	1	0	1	1	0	0	0	0	0	1
19	10159625	10159703	79	Q3_del	1	0	1	1	0	0	0	0	0	1
19	10240669	10240871	203	H2_del	1	0	1	1	0	1	1	0	0	1
19	10402703	10402732	30	H2_del	1	1	1	1	0	1	1	0	0	1
19	10421825	10421854	30	Q7_del	1	1	1	1	0	1	1	0	0	1
19	10428847	10428891	45	H1_del	1	1	1	1	0	1	1	0	0	1
19	10429999	10430038	40	Q3_del	1	1	1	1	0	1	1	0	0	1
19	10446239	10446268	30	H1_del	1	1	1	1	0	1	1	0	0	1
19	10488619	10488649	31	H1_del	0	0	0	0	0	1	0	0	0	1
19	10543222	10543251	30	H2_del	1	1	1	1	0	1	1	0	0	1
19	10580942	10580982	41	H2_del	1	1	1	1	0	1	1	0	0	2
19	10580942	10580982	41	H2_del	1	1	1	1	0	1	1	0	0	2
19	10583655	10584333	679	Q7_del	1	1	1	1	0	1	1	0	0	1
19	10747303	10747557	255	Q7_del	1	0	0	0	0	0	0	0	0	1
19	10805972	10806022	51	H2_del	0	0	0	1	0	1	1	1	0	1
19	10818934	10818985	52	H2_del	0	0	0	1	0	1	1	0	0	1
19	10823180	10823217	38	H1_del	0	0	0	1	0	1	1	0	0	1
19	10839666	10839718	53	H2_del	1	0	0	1	0	1	1	0	0	2
19	10839666	10839718	53	H2_del	1	0	0	1	0	1	1	0	0	2
19	10962866	10962895	30	H2_del	0	0	0	1	0	1	1	0	0	1
19	11860350	11860455	106	H1_del	1	0	1	0	0	0	0	0	0	1
19	12017607	12017641	35	H2_del	0	0	0	1	0	1	1	0	0	1
19	12023742	12023839	98	H2_del	1	0	1	1	0	1	1	0	0	1
19	12025562	12025618	57	H2_del	1	0	1	1	0	1	1	0	0	1
19	12026022	12026114	93	H1_del	1	0	1	1	0	1	1	0	0	1

19	12278946	12279004	59	H2_del	0	0	2	1	0	1	1	0	0	1
19	12346453	12346520	68	H2_del	1	0	1	0	0	0	0	0	0	1
19	12358650	12358738	89	H1_del	1	0	1	0	0	0	0	0	0	1
19	13075520	13075592	73	H2_del	1	0	1	0	0	0	0	0	0	1
19	15011724	15012393	670	Q7_del	0	1	0	0	0	0	0	0	0	2
19	15011724	15012393	670	Q7_del	0	1	0	0	0	0	0	0	0	2
19	15219993	15227269	7277	Q6_del	0	1	0	0	0	0	0	0	0	2
19	15219993	15227269	7277	Q6_del	0	1	0	0	0	0	0	0	0	2
19	15980612	15981451	840	Q6_del	0	0	0	0	0	0	0	0	0	1
19	16875697	16876189	493	Q7_del	0	0	0	0	0	1	1	0	0	1
19	17060025	17060026	300	H7_ins	0	1	1	0	0	0	0	0	0	1
19	17320034	17320138	105	Q7_del	1	1	1	1	0	2	2	2	0	1
19	17320684	17321987	1304	H1_del	1	1	1	1	0	na	na	na	0	1
19	17366946	17367281	336	Q7_del	1	1	1	1	0	2	2	1	0	2
19	17366946	17367281	336	Q7_del	1	1	1	1	0	2	2	1	0	2
19	17504253	17504536	284	Q7_del	0	0	1	0	0	1	1	0	0	1
19	18868336	18868642	307	Q7_del	0	1	0	0	0	0	0	0	0	1
19	19888771	19889453	683	Q3_del	0	1	1	0	0	0	1	1	0	1
19	19984774	19984867	94	Q2_del	1	1	1	1	0	1	1	1	0	1
19	20221005	20221026	>2000	H7_ins	0	1	1	0	0	0	0	0	0	1
19	20548784	20550670	1887	Q3_del	1	1	1	1	0	1	1	1	0	1
19	20864778	20865232	455	Q5_del	1	0	1	0	0	1	0	0	0	1
19	21574928	21575536	609	Q5_del	1	1	1	0	0	0	0	1	0	1
19	21672455	21673238	784	Q5_del	0	1	0	0	0	0	0	1	0	1
19	21678008	21678269	262	Q7_del	0	0	0	0	0	0	0	1	0	1
19	21992466	21992586	121	H2_del	0	0	0	1	0	1	1	1	0	1
19	22011683	22013072	1390	Q2_del	1	1	1	1	0	1	1	1	0	1
19	22401821	22402446	626	Q2_del	1	1	1	0	0	0	0	1	0	1
19	22662688	22663093	406	Q3_del	1	1	1	1	0	1	1	1	0	1
19	22961240	22961818	579	Q7_del	0	2	0	1	0	1	1	0	0	2
19	22961240	22961818	579	Q7_del	0	2	0	1	0	1	1	0	0	2
19	23386219	23386229	373	H7_ins	0	0	0	1	0	1	1	0	1	1
19	23867733	23867924	192	Q1_del	1	1	0	1	0	1	1	0	0	1
19	23913565	23914061	497	Q7_del	1	1	1	2	0	2	2	1	0	1
19	24438910	24439500	591	Q7_del	0	0	1	1	0	1	1	0	0	2
19	24438910	24439500	591	Q7_del	0	0	1	1	0	1	1	0	0	2
19	24986698	24993713	7016	Q3_del	1	1	2	2	0	2	2	0	0	1
19	25131982	25132090	109	Q7_del	1	1	2	1	0	1	1	0	0	1
19	25223059	25223506	448	Q7_del	0	0	0	1	0	1	1	0	0	1
19	25277993	25278210	218	Q1_del	1	0	1	0	0	0	0	0	0	1
19	25387968	25388226	259	Q7_del	0	0	0	1	0	1	0	2	0	1
19	25445519	25446718	1200	Q2_del	1	0	1	0	0	0	0	1	0	1
19	25711143	25711514	372	Q1_del	0	0	0	1	0	1	1	1	0	1
19	25885993	25886393	401	Q1_del	0	2	0	2	0	2	2	1	0	1
19	26114707	26115669	963	Q5_del	1	1	0	1	0	1	1	0	0	2
19	26114707	26115669	963	Q5_del	1	1	0	1	0	1	1	0	0	2
19	27166922	27167565	644	Q7_del	0	1	0	0	0	0	0	0	0	1
19	27785834	27789921	4088	Q3_del	0	0	0	0	0	0	0	1	0	1
19	28291845	28292682	838	Q3_del	1	0	0	0	0	0	0	0	0	1
19	28316426	28316948	523	Q1_del	1	0	0	0	0	0	0	0	0	1
19	28620807	28620970	164	Q7_del	1	0	0	0	0	0	0	0	0	1
19	29525287	29525849	563	Q7_del	0	0	0	0	0	0	0	0	0	1
19	30058259	30058489	231	Q7_del	0	1	0	1	0	1	1	1	0	1
19	30941798	30942361	564	Q3_del	0	0	0	0	0	0	0	1	0	1
19	31503801	31504276	476	H2_del	0	0	0	0	0	0	0	1	1	1
19	34767448	34767610	163	Q3_del	1	0	1	0	0	0	0	0	0	1
19	35166544	35166983	440	Q7_del	1	0	1	0	0	0	0	0	0	1
19	37669327	37669798	472	Q7_del	1	1	1	1	0	1	1	1	0	1
19	38122102	38122721	620	Q5_del	1	1	1	1	0	1	1	1	0	1
19	38122405	38122406	178	H6_ins	1	1	1	1	0	1	1	1	1	1
19	38902989	38903279	291	Q7_del	1	1	1	1	0	1	1	1	0	1
19	38926596	38927257	662	Q7_del	1	1	1	1	0	1	1	1	0	1
19	40296944	40297520	577	Q6_del	0	0	0	0	0	0	0	0	0	1
19	40582918	40583348	431	Q1_del	1	1	1	1	0	1	1	1	0	1

19	41004153	41004751	599	Q5_del	1	1	1	0	0	0	0	1	0	1
19	41004606	41004610	97	H6_ins	1	1	1	0	0	0	0	1	1	1
19	41947577	41947725	149	Q7_del	1	1	1	1	0	1	1	1	0	1
19	42634730	42635821	1092	Q5_del	1	1	1	1	0	1	1	1	0	1
19	42634792	42635366	575	Q5_del	1	1	1	1	0	1	1	1	0	2
19	42634792	42635366	575	Q5_del	1	1	1	1	0	1	1	1	0	2
19	42639692	42640094	403	Q7_del	1	1	1	1	0	1	1	1	0	1
19	43882576	43882797	222	Q7_del	1	1	2	1	0	2	1	1	0	1
19	44194931	44195258	328	Q7_del	2	1	2	3	0	2	2	1	0	1
19	44405427	44405959	533	Q7_del	0	1	0	1	0	1	0	0	0	1
19	45137645	45138318	674	Q5_del	0	0	0	1	0	1	0	1	0	1
19	45205757	45206387	631	H1_del	0	1	0	1	0	1	0	0	1	1
19	45277248	45280317	3070	Q3_del	1	1	1	0	0	0	1	1	0	1
19	45398634	45399165	532	Q5_del	1	1	1	0	0	0	1	1	0	1
19	45446593	45447114	522	Q6_del	0	0	0	0	0	0	0	0	0	1
19	46625053	46625127	75	Q2_del	1	1	1	1	0	1	1	1	0	1
19	46793212	46793658	447	Q7_del	1	1	1	1	0	1	1	0	0	1
19	47664890	47677127	12238	Q3_del	0	1	0	0	0	0	0	0	0	1
19	48061057	48061892	836	Q2_del	1	0	1	0	0	0	1	1	0	1
19	48128646	48129210	565	Q7_del	1	1	1	1	0	1	1	1	0	1
19	50709722	50709857	136	Q1_del	1	1	1	0	0	0	1	1	0	1
19	50785953	50786012	60	Q7_del	1	1	1	0	0	0	1	1	0	1
19	50922889	50924627	1739	Q2_del	1	0	1	0	0	0	0	0	0	1
19	50937949	50940477	2529	H2_del	1	1	1	0	0	0	0	1	1	1
19	50965819	50966879	1061	H2_del	1	1	1	0	0	0	0	1	0	1
19	50982182	50983101	920	H2_del	1	1	1	0	0	0	0	1	1	1
19	53018379	53019936	1558	Q9_inv	1	0	1	1	0	1	1	1	0	1
19	55137466	55137837	372	Q1_del	1	1	1	1	0	1	1	1	0	1
19	55442803	55443554	752	Q7_del	0	1	0	1	0	1	1	1	0	1
19	56563375	56563472	98	Q7_del	0	1	0	0	0	0	0	0	0	1
19	56871252	56871702	451	Q7_del	0	1	0	1	0	0	0	0	0	1
19	57325727	57325911	185	Q1_del	0	1	1	1	0	1	1	1	0	2
19	57325727	57325911	185	Q1_del	0	1	1	1	0	1	1	1	0	2
19	58357817	58358384	568	Q7_del	1	2	1	1	0	1	1	1	0	2
19	58357817	58358384	568	Q7_del	1	2	1	1	0	1	1	1	0	2
19	59423833	59425976	2181	H8_dup	0	0	0	1	0	1	1	0	1	1
19	59496174	59496440	267	Q7_del	1	1	1	1	0	1	1	1	0	1
19	59554960	59555092	133	Q1_del	1	1	1	1	0	1	1	1	0	1
19	60059361	60059499	139	H1_del	1	0	0	1	0	1	1	1	1	1
19	60181101	60181439	339	Q8_inv	1	1	1	1	0	1	1	0	0	1
19	60693637	60694054	418	Q3_del	1	1	1	1	0	1	1	1	0	1
19	60848923	60849421	499	Q6_del	1	1	1	1	0	1	1	0	0	1
19	60928887	60929139	253	Q7_del	1	1	1	1	0	1	1	1	0	1
19	60954709	60956373	1665	H1_del	0	1	1	1	0	1	1	0	0	1
X	36234184	36234343	>2000	H7_ins	0	0	0	0	0	0	0	1	0	1
X	93130993	93152177	21185	Q6_del	1	1	1	1	0	1	1	1	0	2
X	93130993	93152177	21185	Q6_del	1	1	1	1	0	1	1	1	0	2
X	117454414	117454437	>2000	H7_ins	1	0	1	1	0	1	0	0	0	1
X	152736226	152736253	4000	H7_ins	1	0	1	0	0	0	0	0	0	1

Complete PCR data set: Col1 indicates the chromosome, col2-3 the start and end coordinates (in Bp). Col4 is the length of the structural variant (in Bp). Col5 is the PEM pattern. Col6-13 indicate presence (=1) or absence (=0) of the SV in the eight founder strains of the HS population (A/J, AKR/J, BALB/cJ, C57BL/6N, CBA/J, DBA/2J and LP/J). Multiallelic SVs are indicated using "1", "2", "3" or "4". Col14 indicates whether or not the region has been resolved to nucleotide level resolution, with "1" meaning yes and "0" meaning no. When col14 ="1", col2-3 refer to the exact coordinates, otherwise they are estimates using LookSeq. Col15 is the primer coverage (number of primer pairs designed per unique SV site).

Supplementary Table 5a

| Strain | Mean (bp) | | Median (bp) | | Total Deletions |
	5' Diff.	3' Diff	5' Diff	3' Diff	
A/J	-175	+14	0	0	100
AKR/J	-45	-23	0	0	97
BALB/cJ	-613	-22	0	0	93
C3H/HeJ	-35	+14	0	0	116
C57BL/6N	-	-	-	-	0
CBA/J	-70	0	0	0	108
DBA/2J	+33	+7	0	0	108
LP/J	-815	+187	0	0	90

Assessment of the accuracy of deletion breakpoints derived from local assembly and breakpoint refinement. Comparisons were made to deletion breakpoints (H1-H3_del, Q1-Q3_del, Q4_del and Q7_del) characterized by PCR and Sanger sequencing (see Supplementary Table 4) for deletions >=100bp. The 5' and 3' breakpoints were assessed independently; the mean and median distance from the actual breakpoints are shown, where '-' is upstream of the actual breakpoint, and '+' is downstream. Overall, the mean difference for 1424 breakpoints (from 712 deletions) is -98 bp and the median is 0bp (85.7% of breakpoints are less than 20 bp from the actual breakpoint; 56.9% are exact).

Supplementary Table 5b

| Strain | Mean (bp) | | Median (bp) | | Total Deletions |
	5' Diff.	3' Diff	5' Diff	3' Diff	
A/J	-1712	+8530	-20.5	+2	16
AKR/J	-3473	-409	-39.5	+9	14
BALB/cJ	-2052	+6096	-59.5	+2.5	14
C3H/HeJ	-1504	+1185	-56	+17	18
C57BL/6N	-	-	-	-	0
CBA/J	-1723	+1223	-36	+2	15
DBA/2J	-1872	+1985	-4	+4.5	14
LP/J	-2984	+3232	-50	+9	18

Assessment of the accuracy of deletion breakpoints derived from raw deletion breakpoint calls. In these cases, local assembly and breakpoint refinement failed to find the breakpoints, but a loss in read coverage and PEM patterns provided evidence for a deletion. Comparisons were made to deletion breakpoints (H1-H3_del, Q1-Q3_del, Q4_del and Q7_del) characterized by PCR and Sanger sequencing for deletions >=100bp. The 5' and 3' breakpoints were assessed independently; the mean and median distance from the actual breakpoints are shown, where '-' is upstream of the actual breakpoint, and '+' is downstream. Overall, the mean difference for 218 breakpoints (from 109 deletions) is 477 bp and the median is -1 bp (only 34.0% of breakpoints are less than 20 bp from the actual breakpoint; 2.3% are exact. However, 75.7% are within 150 bp of the actual breakpoint).

Supplementary Table 5c

	Mean (bp)		Median (bp)		
Strain	**5' Diff.**	**3' Diff**	**5' Diff**	**3' Diff**	**Total Insertions**
A/J	1	0	0	0	13
AKR/J	1	-3	0	0	7
BALB/cJ	1	61	0	0	9
C3H/HeJ	0	46	0	0	12
C57BL/6N	-	-	-	-	0
CBA/J	+1	+51	0	0	11
DBA/2J	0	+1	0	0	11
LP/J	+1	+93	0	0	6

Assessment of the accuracy of insertion breakpoints derived from local assembly and breakpoint refinement. Comparisons were made to insertion breakpoints (H6_ins and Q9_inv) identified from PCR and Sanger sequencing. Insertion breakpoints from the computational analysis may be given as a small range rather than a single coordinate, therefore the 5' and 3' breakpoints each assessed against the actual breakpoint. Shown are the mean and median distance (bp) from the actual breakpoint, where '-' is upstream of the actual breakpoint, and '+' is downstream.

Supplementary Table 5d

	Mean (bp)		Median (bp)		Total
Strain	**5' Diff.**	**3' Diff**	**5' Diff**	**3' Diff**	**H4/H5**
A/J	+10/-4	-44/-1	+5/-5	-50/0	3/5
AKR/J	-8/-18	-45/-6	-9/-17	-46/-7	1/3
BALB/cJ	-14/-4	-72/-8	-15/-5	-73/-11.5	1/4
C3H/HeJ	+30/+46	-33/-8	+0.5/-2	-10/-10	4/5
C57BL/6N	-	-	-	-	-
CBA/J	0/+44	-50/-10	0/8	-51/0	1/3
DBA/2J	+4/0	-36/+3	0/-2	-14.5/4	4/3
LP/J	-8/+29	-26/-21	-20/+29	-11/-22	3/2

Assessment of breakpoint localization accuracy of inversions and inversions with deletions (H4_inv and H5_inv). Comparisons were made between insertion breakpoints identified from PCR and Sanger sequencing and inversion breakpoints determined from analysis of PEM patterns only, not local assembly.

Supplementary Table 5e

Strain	Mean (bp)		Median (bp)		
	5' Diff.	3' Diff	5' Diff	3' Diff	Total
A/J	+5	+8	+5	-3	4
AKR/J	+15	-20	+18	-22	3
BALB/cJ	+3	-10	+3	-11	1
C3H/HeJ	+8	-33	+8	-34	1
C57BL/6N	-	-	-	-	0
CBA/J	+21	-6	+21	-7	2
DBA/2J	+8	-11	-7.5	-11.5	2
LP/J	+15	-18	0	-18	3

Assessment of breakpoint localization accuracy of tandem duplications (H8_dup). Comparisons were made between tandem duplications identified from PCR and Sanger sequencing and those discovered from analysis of PEM patterns only, not local assembly.